

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 14:04:54 ; Search time 2174 Seconds
(without alignments)
9451.049 Million cell updates/sec

Title: US-09-912-628-4
Perfect score: 706
Sequence: 1 ggcacgagctctctctctg.....gtaaaaaaaaaaaaaaaa 706

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
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- 3: gb.in.*
- 4: gb.om.*
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- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
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- 12: gb.sy.*
- 13: gb.vi.*
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- 15: em.ba.*
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- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
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- 22: em.ox.*
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- 27: em.sts.*
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- 29: em.vi.*
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- 32: em.htg_other.*
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- 34: em.htg_pln.*
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- 36: em.htg_rod.*
- 37: em.htg_vrt.*
- 38: em.ey.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	250.4	35.5	695	6	AX147521	Sequence
2	250.4	35.5	868	6	AX147520	Sequence
3	250.4	35.5	1302	6	AX147519	Sequence
4	249.2	35.3	1366	6	AX147518	Sequence
5	248.4	35.2	1365	6	AK098566	Homo sapi
6	247.2	35.0	1361	9	HSTHRINH	222658 H. sapiens t
7	246.8	35.0	1324	6	AX147509	Sequence
8	246.8	35.0	1349	6	AX147468	Sequence
9	246.8	35.0	1410	6	AX147508	Sequence
10	246.8	35.0	1465	6	AX147508	Sequence
11	246.8	35.0	1465	9	S69272	cytoplasmic
12	246.8	35.0	1523	9	BC001394	Homo sapi
13	246.8	35.0	2036	9	AK094983	Homo sapi
14	246.8	35.0	3271	9	AK057138	Homo sapi
15	245.2	34.7	2759	9	AK027149	Homo sapi
16	244	34.6	1327	4	D55670	Bos taurus
17	237.8	33.7	1317	10	MMU25844	Mus muscu
18	236.6	33.5	1532	10	BC006766	Mus muscu
19	225.4	31.9	1859	10	U96707	Mus muscu
20	218	30.9	1265	10	AF425084	Mus muscu
21	214.4	30.4	311	6	AX186945	Sequence
22	214.4	30.4	1319	9	BC034528	Homo sapi
23	214.4	30.4	1325	9	HUMCAP2A	Homo sapi
24	214.4	30.4	1425	6	AR005195	Sequence
25	214.4	30.4	1425	6	AR005195	Sequence
26	214.4	30.4	1425	6	AR005195	Sequence
27	212.4	30.1	922	9	HSU92984	Homo sapien
28	206	29.2	186351	2	AP001503	Homo sapi
29	206	29.2	191395	9	AC009802	Homo sapi
30	206	29.2	191793	2	AP001897	Homo sapi
31	206	29.2	198231	2	AC067875	Homo sapi
32	206	29.2	201734	2	AC090224	Homo sapi
33	196.8	27.9	287	6	AX185519	Sequence
34	179.2	25.4	1626	9	HSU71364	Human serin
35	178.8	25.3	1413	10	U96703	Mus muscu
36	178.8	25.3	1779	10	BC025121	Mus muscu
37	177.4	25.1	1385	9	HUMCAP3A	Homo sapien
38	177.4	25.1	1393	6	AR005196	Sequence
39	177.4	25.1	1393	6	AR005196	Sequence
40	177.4	25.1	1393	6	AR005196	Sequence
41	177.4	25.1	2792	9	AB060690	Sequence 3
42	177.4	25.1	4130	9	BC002538	Homo sapi
43	167.4	23.7	1819	10	U96700	Mus muscu
44	167.4	23.7	2283	10	BC029900	Mus muscu
45	152.4	21.6	1931	10	U96705	Mus muscu

ALIGNMENTS

RESULT 1	AX147521	Sequence 75 from Patent WO0136632.	695 bp	DNA	linear	PAT 08-JUN-2001
LOCUS	AX147521	Sequence 75 from Patent WO0136632.	695 bp	DNA	linear	PAT 08-JUN-2001
DEFINITION	AX147521	Sequence 75 from Patent WO0136632.	695 bp	DNA	linear	PAT 08-JUN-2001
ACCESSION	AX147521	Sequence 75 from Patent WO0136632.	695 bp	DNA	linear	PAT 08-JUN-2001
VERSION	AX147521.1	GI:14346678	695 bp	DNA	linear	PAT 08-JUN-2001
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 695)					
AUTHORS	Levine, Z., David, A., Azar, I., Khosravi, R. and Bernstein, J.					
TITLE	Varian of alternative splicing					
JOURNAL	Patent: WO 0136632-A 75 25-MAY-2001					

Db	60	CTTGGGCTGCCCATCATGGATGTTCTCGCAGAAGCAAAATGGCACCTTTGCCTTAAACCTT	119
Qy	97	TTGAAAAAGCTAGGGGAAAAACAACCTCAAACTATTTTTC-CCCATGAGCATATCA	155
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Qy	156	TCAGCCTTGGCCATGGTTTTCATGGGGCAAAAGGAAACACTGCGAGTCTAGTCTCAG	215
Db	180	TGTGCCCTGGCCATGGTCTACATGGGGCAAAAGGAAACACTGCGAGTCTAGTCTCAG	239
Qy	216	GCACTTTGTTTGTAGTAAATCGGAGGTGAAGATGAGATATTCATCGAGTCTTTCAGTCA	275
Db	240	ATACTTTCTTCAATAAAGTGGCGGT---GGTGGAGACATCCACAGGGCTTTCAGTCT	296
Qy	276	CTTCTTTGTTGCAATTAACAGAACTGACACTGAATATGTCTTAGAACTGCCAACGGGCTC	335
Db	297	CTTCTCACCGAAGTGAACAGACTGCGACGCGACTTCTTCTAGGATGGCCAAAGGCTC	356
Qy	336	TTTGGAGAAAAGTCTTATGATTTCTCCACAGGTTTTCAGATTTCTGTGGCAATTTCTAC	395
Db	357	TTTGGGAAAAGTCTTGTGATTTCTCTCATCTTTTAGAGATTTCTTCCCAAAATTTCTAC	416
Qy	396	CAAGCAACGATAAAACAGCTAGACTTTGTGAATGATACAGAGAAAGTCCCAACAGCTGA	455
Db	417	CAAGCAGAGATGGAGGAGCTTGACTTTTATCAGCGCGGTAGAGAGTCCAGAAAACACATA	476
Qy	456	AACCTCTCTGGTGTCTGATAAACTAAAG	483
Db	477	AACACCTGGGTAGCTGAAAGACAGAG	504
RESULT 3			
LOCUS	AX147519	1302 bp	DNA linear PAT 08-JUN-2001
DEFINITION	Sequence 73 from Patent WO0136632.		
ACCESSION	AX147519		
VERSION	AX147519.1	GI:14346676	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1302)		
AUTHORS	Levine, Z., David, A., Azar, I., Khosravi, R. and Bernstein, J.		
TITLE	Variants of alternative splicing		
JOURNAL	Patent: WO 0136632-A 73 25-MAY-2001;		
FEATURES	CompuGen Ltd. (IL)		
source	1. 1302		
BASE COUNT	341 a	305 c	345 g 311 t
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	/db_xref="taxon:9606"		
Query Match	35.5%	Score 250.4;	DB 6; Length 1302;
Best Local Similarity	75.4%;	Pred. No. 8.4e-61;	
Matches	338; Conservative	0; Mismatches 106;	Indels 4; Gaps 2;
Qy	37	CTGGGGCTCACCGTCTATGATGCTCTATCAGAAGCAAAATGGCAATTTGCAATTAACCTT	96
Db	60	CTTGGGCTGCCCATCATGGATGTTCTCGCAGAAGCAAAATGGCACCTTTGCCTTAAACCTT	119
Qy	97	TTGAAAAAGCTAGGGGAAAAACAACCTCAAACTATTTTTC-CCCATGAGCATATCA	155
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Qy	156	TCAGCCTTGGCCATGGTTTTCATGGGGCAAAAGGAAACACTGCGAGTCTAGTCTCAG	215
Db	180	TGTGCCCTGGCCATGGTCTACATGGGGCAAAAGGAAACACTGCGAGTCTAGTCTCAG	239
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Qy	276	CTTCTTTGTTGCAATTAACAGAACTGACACTGAATATGTCTTAGAACTGCCAACGGGCTC	335
Db	297	CTTCTCACCGAAGTGAACAGACTGCGACGCGACTTCTTCTAGGATGGCCAAAGGCTC	356
Qy	336	TTTGGAGAAAAGTCTTATGATTTCTCCACAGGTTTTCAGATTTCTGTGGCAATTTCTAC	395
Db	357	TTTGGGAAAAGTCTTGTGATTTCTCTCATCTTTTAGAGATTTCTTCCCAAAATTTCTAC	416
Qy	396	CAAGCAACGATAAAACAGCTAGACTTTGTGAATGATACAGAGAAAGTCCCAACAGCTGA	455
Db	417	CAAGCAGAGATGGAGGAGCTTGACTTTTATCAGCGCGGTAGAGAGTCCAGAAAACACATA	476
Qy	456	AACCTCTCTGGTGTCTGATAAACTAAAG	483
Db	477	AACACCTGGGTAGCTGAAAGACAGAG	504
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LOCUS	AX147520	868 bp	DNA linear PAT 08-JUN-2001
DEFINITION	Sequence 74 from Patent WO0136632.		
ACCESSION	AX147520		
VERSION	AX147520.1	GI:14346677	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 868)		
AUTHORS	Levine, Z., David, A., Azar, I., Khosravi, R. and Bernstein, J.		
TITLE	Variants of alternative splicing		
JOURNAL	Patent: WO 0136632-A 74 25-MAY-2001;		
FEATURES	CompuGen Ltd. (IL)		
source	1. 868		
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AK098566
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
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 Homo sapiens testis cDNA to mRNA, clone_lib:TST04708.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,
 Arita, M., Muraashino, K., Yuuki, H., Hara, H., Suzuki, Y., Hata, H.,
 Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T.,
 Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A.,
 Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 1565)
 Sugano, S. and Suzuki, Y.
 Direct Submission
 Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science,
 University of Tokyo, Laboratory of Genome Structure, Human Genome
 Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
 (E-mail: cdnal@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,
 Fax: 81-3-5449-5416)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction and 5'-end one pass sequencing: Institute of Medical
 Science, University of Tokyo, Laboratory of Genome Structure, Human
 Genome Center; 3'-end one pass sequencing: RAB; clone selection for
 full insert sequencing: RAB and Helix Research Institute.
FEATURES
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 /db_xref="taxon:9606"
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 BASE COUNT 390 a 381 c 428 g 366 t
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 Best Local Similarity 76.0%; Pred. No. 3.2e-60;
 Matches 333; Conservative 0; Mismatches 101; Indels 4; Gaps 2;
 QY 47 CCGTCATGGATGCTCTATCAGAAGCAATGGCACATTTGCATTAACCTTTTGAAAAAGC 106
 Db 296 CCATCATGGATGTTCTCGCAGAAGCAATGGCACCTTTGCCTTAAACCTTTGAAAAGC 355
 QY 107 TAGGGGAAACAACTCAACAACCTATTATTTTTC-CCCATGAGCATATCATCAGCCTGG 165
 Db 356 TGGGTAAGAGCAACTCGAAGATGTGTTTTCTCACCCATGAGCATGCTGTGCCCTGG 415
 QY 166 CCATGGTTTTTCATGGGGGCAAGGAAACACTGCGAGCTCAGATGCTCAGGCACCTTGG 225
 Db 416 CCATGGTCTACATGGGGGCAAGGAAACACCGCTGCACAGATGCCCGCATCTTCTT 475
 QY 226 TTAGTAAATCGGAGGTGAAGATGGAGATATTTCATCGAGGTTTTTCAGTCACCTTCTTGTG 285
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 QY 286 CAATTAAACAGAACTGACACTGNATATGTGCTTAGNACTGCCAAGCGGCTCTTTGGAGAA 345
 Db 533 AAGTGAACAAGCTGGCAGCAGTACTTGCTTAGATGCGCAACAGGCTCTTTGGGAAA 592

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LOCUS H.sapiens thrombin inhibitor mRNA.
DEFINITION Z22658
ACCESSION Z22658.1 GI:297411
VERSION thrombin inhibitor.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1361)
Coughlin,P., Sun,J., Cerruti,L., Salem,H.H. and Bird,P.
Cloning and molecular characterization of a human intracellular
serine proteinase inhibitor
Proc. Natl. Acad. Sci. U.S.A. 90 (20), 9417-9421 (1993)
JOURNAL 94022386
MEDLINE 8415716
PUBMED 2 (bases 1 to 1361)
REFERENCE Steinle,A.
AUTHORS Direct Submission
TITLE Submitted (27-APR-1993) Steinle A., University of Munich, Institute
JOURNAL of Immunology, Goethestrasse 31, W-8000 MUENCHEN 2, GERMANY
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Best Local Similarity 75.0%; Pred. No. 7e-60;
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QY 97 TTGAAAAAGCTAGGGGAAAAACAACCTCAAAACAACCTTATTTTTTTC-CCCATGAGCATATCA 155
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RESULT 7
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LOCUS Sequence 63 from Patent WO0136632.
DEFINITION AX147509
ACCESSION AX147509
VERSION AX147509.1 GI:14346666
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1324)
Levine,Z., David,A., Azar,I., Khosravi,R. and Bernstein,J.
Variants of alternative splicing
Patent: WO 0136632-A 63 25-MAY-2001;
Compugen Ltd. (IL)
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/db_xref="taxon:9606"
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Best Local Similarity 75.8%; Pred. No. 9.1e-60;
Matches 332; Conservative 0; Mismatches 102; Indels 4; Gaps 2;
QY 47 CCGTCATGATGCTCTATCAGAACCAATGGCAATTCGACATTAACCTTTTGAAGAACG 106
Db 204 CCATCATGATGTTCTTCAGAGCAAAATGGCAACCTTTTGCCTTAACCTTTTGAAGAACG 263
QY 107 TAGGGGAAAAACAACCTCAAAACAACCTTATTTTTTTC-CCCATGAGCATATCATCAGCCTTG 165
Db 264 TGGGTAAAGCAACCTCGAAGATGTGTTTTTCTCACCATGAGCATGCTGTGCGCTGG 323
QY 166 CCATGGTTTTTCATGGGGGCAAGGAAACACTGAGCTCAGATGTCTCAGGACATTTGT 225
Db 324 CCATGGTCTACATGGGGGCAAGGAAACACCCGCTGCACAGATGGCCCATGACTTCTT 383
QY 226 TTAGTAAATCGAGGTGAAGATGAGATATTATTCAGAGGTTTTTCAGTCACATCTTTGTG 285
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QY 286 CAATTAACAGAACTGACACTGAATATGTGCTTAGAACTGCCCAAGGGCTCTTTGGAGAA 345

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 QY 346 AGTCTTATGATTTCTTCACAGGTTTACAGATTCCTGTGGCAAAATTTACCAAGCAAGA 405
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 QY 406 TAAACAGCTAGACTTTGTGAATGATACAGAGAAAGTCCACAAACAGCTGTAAACTCCCTGGG 465
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 QY 466 TTGCTGATAAACTAAAG 483
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 DEFINITION
 ACCESSION
 AX147468
 VERSION
 AX147468.1 GI:14346625
 KEYWORDS
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 Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1349)
 Levine, Z., David, A., Azar, I., Khosravi, R. and Bernstein, J.
 Variants of alternative splicing
 Patent: WO 0136632-A 22 25-MAY-2001;
 Compugen Ltd. (IL)
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 Matches 332; Conservative 0; Mismatches 102; Indels 4; Gaps 2;
 QY 47 CCGTCATGATGCTCTATCAGAGCAAAATGGCAATTTGCAATTAACCTTTTGAAGAACG 106
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RESULT 9
 AX147508
 LOCUS
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 ACCESSION
 AX147508
 VERSION
 AX147508.1 GI:14346665
 KEYWORDS
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 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1410)
 Levine, Z., David, A., Azar, I., Khosravi, R. and Bernstein, J.
 Variants of alternative splicing
 Patent: WO 0136632-A 62 25-MAY-2001;
 Compugen Ltd. (IL)
 FEATURES
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 376 a 390 g 333 t 1 others
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Db 621 TAGCTGAAGACAGAGAAG 638

RESULT 9
 AX147508
 LOCUS
 DEFINITION
 ACCESSION
 AX147508
 VERSION
 AX147508.1 GI:14346665
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1410)
 Levine, Z., David, A., Azar, I., Khosravi, R. and Bernstein, J.
 Variants of alternative splicing
 Patent: WO 0136632-A 62 25-MAY-2001;
 Compugen Ltd. (IL)
 FEATURES
 Location/Qualifiers
 1..1410
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 376 a 390 g 333 t 1 others
 ORIGIN

Query Match 35.0%; Score 246.8; DB 6; Length 1410;
 Best Local Similarity 75.8%; Pred. No. 9.1e-60;
 Matches 332; Conservative 0; Mismatches 102; Indels 4; Gaps 2;
 QY 47 CCGTCATGATGCTCTATCAGAGCAAAATGGCAATTTGCAATTAACCTTTTGAAGAACG 106
 Db 204 CCATCATGATGTTCTCGCAGAGCAAAATGGCACTTTGGCCTTAAACCTTTTGAAGAACG 263
 QY 107 TAGGGGAAAACAACTCAAACTTATTTTTC-CCCATGAGCATATCATCAGCCTTGG 165
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 QY 166 CCATGTTTTCATGGGGCAAGGCAAACTGCAATTCAGATGCTCAGGCACTTTGTT 225
 Db 324 CCATGTTCTACATGGGGCAAGGCAAACTGCAATTCAGATGCTCAGGCACTTTGTT 285
 QY 226 TTAGTAAATTCGAGGTTGAAGATGAGATATTCATCGAGGTTTTCAGTCACTTTCTT 383
 Db 384 TCAATAAAGTGGCGGT---GGTGGAGACATCCACAGGCTTCCAGTCTCTTCTCACCG 440
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 Db 441 AAGTGAACAGACTGGCAGCAGTACTTGGTGGCCCAACAGGCTCTTTGGGAAA 500
 QY 346 AGTCTTATGATTTCTTCACAGGTTTACAGATTCCTGTGGCAAAATTTTACCAAGCAAGA 405
 Db 501 AGTCTTGTGATTTCTCTCATCTTTTAGAGATTCCTGCCAAAATTTTACCAAGCAGAGA 560
 QY 406 TAAACAGCTAGACTTTGTGAATGATACAGAGAAAGTCCACAAACAGCTGTAAACTCCCTGGG 465
 Db 561 TGGAGGAGCTTGACTTTATCAGCGCGGTAGAGAGTCCAGAAAACATATAACACCTGGG 620
 QY 466 TTGCTGATAAACTAAAG 483
 Db 621 TAGCTGAAGACAGAGAAG 638

RESULT 10
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 LOCUS
 DEFINITION
 ACCESSION
 AX410381
 VERSION
 AX410381.1 GI:21443086
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1465)
 Levine, Z., David, A., Azar, I., Khosravi, R. and Bernstein, J.
 Variants of alternative splicing
 Patent: WO 0136632-A 62 25-MAY-2001;
 Compugen Ltd. (IL)
 FEATURES
 Location/Qualifiers
 1..1465
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 3028 a 3028 g 1465 bp DNA
 ORIGIN

entry [NCBI gibbsq 145231] from the original journal article.
This sequence comes from Fig. 1.

REFERENCE	Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
AUTHORS	
TITLE	Gene expression profiles in liver cancer
JOURNAL	Patent: WO 0229103-A 3028 11-APR-2002;
	GENE LOGIC INC (US)
FEATURES	
source	Location/Qualifiers
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	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/notes="EMBL/GenBank Accession No. S69272"
BASE COUNT	397 a 331 c 392 g 345 t
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	Query Match 35.0%; Score 246.8; DB 6; Length 1465;
	Best Local Similarity 75.8%; Pred. No. 9.1e-60;
	Matches 332; Conservative 0; Mismatches 102; Indels 4; Gaps 2;
QY	47 CCGTCATGGATGCTCTATCAGAGCAAAATGGCAATTTGCAATTAACCTTTTGAAGAACG 106
Db	184 CCATCATGGATGTTCTCGCAGAGCAAAATGGCAATTTGCCCTTAACCTTTTGAAGAACG 243
	107 TAGGGGAAACCAACTCAAACTTATTTTTC-CCCATGAGCATATCATCAGCTTGG 165
Db	244 TGGGTAAGACAACTCGAGAGATGTTTTCATCCCATGAGCATGCTCTGTCCTGG 303
QY	166 CCATGGTTTTCATGGGGGAAAGGAAACACTGACATGCTCAGATGCTCAGGCACTTTGTT 225
Db	304 CCAATGCTTACATGGGGGAAAGGAAACACCGCTGCAGATGCGCCAGATACCTTTCT 363
QY	226 TTAGTAAATCGAGGTGAGATGAGATATTCATCGAGGTTTTCAGTCACTTCTTGTG 285
Db	364 TCAATAAAGTGGCGGT---GGTGGAGACATCCACAGGGCTTCAGATGCTCTTCTCACCG 420
QY	286 CAATTACAGAACTGACACTGAATATGCTTAAAGCTGCAACCGGCTCTTTGGAGAA 345
Db	421 AAGTGAACAGACTGGCAGCGAGTACTTGTAGGTTGGCCAGCAGGCTCTTTGGGAAA 480
QY	346 AGTCTTATGATTTCTCAGAGTTTACAGATTTCTGTCGCAAAATTTTACCAAGCAAGA 405
Db	481 AGTCTTGTGATTTCT 540
QY	406 TAAACAGCTAGACTTTCTGTAATGATACAGAGAGTCCACAACTGTAACCTCTGGG 465
Db	541 TGGAGAGCTTGACTTTATCAGCGCGGTAGAGAGTCCAGAGAAACACATAAACCTGG 600
QY	466 TTGCTGATAAACTAAAG 483
Db	601 TAGCTGAAAAGACAGAAG 618
RESULT 12	
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LOCUS	cytoplasmic antiproteinase-38 kda intracellular serine proteinase
DEFINITION	inhibitor [human, placenta, mRNA, 1465 nt].
ACCESSION	S69272
VERSION	S69272.1 GI:546087
KEYWORDS	
SOURCE	Homo sapiens placenta.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1465)
AUTHORS	Morgenstern, K.A., Sprecher, C., Holth, L., Foster, D., Grant, F.J.,
TITLE	Ching, A. and Kistiel, W.
	Complementary DNA cloning and kinetic characterization of a novel
	intracellular serine proteinase inhibitor: mechanism of action with
	trypsin and factor Xa as model proteinases
JOURNAL	Biochemistry 33 (11), 3432-3441 (1994)
MEDLINE	94183847
PUBMED	8136380
REMARK	GenBank staff at the National Library of Medicine created this

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1523)
TITLE	Strauberg, R.
JOURNAL	Direct Submission
REMARK	Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapob-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nhgri.nih.gov Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tongson, E.E., Touchman, J.W., Taurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.
FEATURES	Location/Qualifiers 1..1523 /organism="Homo sapiens" /db_xref="LOCUSID:5269" /db_xref="taxon:9606" /clone="MGC:2180 IMAGE:3051381" /issue_type="Colon, adenocarcinoma" /clone_lib="NIH MGC 15" /lab_host="DH10B-R" /note="Vector: pOTB7" 235..1365 /codon_start=1 /product="serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6" /protein_id="AAH01394.1" /db_xref="GI:12655087" /translation="MDVLAENGTFALNLLKTLGKDNKNVFFSPMSMCSALAMVYMG AKNTAAQAQLSLFNKSGGGDIHQGFQSLLEVTNKTGTYLLRVANRLFEKSCDF LSPFSDCKQFYQAEEMELDFISAVEKRKHINTVWAEKTEGKIAELSLSPGVPLTR LVLVNAVPRGNWDQFQKENTFEELFKVSKNEEPQVMPKQSTFKTKYIGELFTOI LVLVYVGLKELNMIIMLPDITDTRVKELETVKEFVETRLDMWDEEREVEVSLPRFKL EESYDMSVLRNLGHTDAFELGKADFGSGSDTSLSKVHKSPFVNEBETEAHAAT AAIMMRCARFVPRCADHPFLFFQHKSTGILFLCGRPSP"
CDS	BASE COUNT 407 a 351 c 405 g 360 t ORIGIN
Query Match	35.0%; Score 246.8; DB 9; Length 1523;
Best Local Similarity	75.8%; Pred. No. 9.1e-60;
Matches 332; Conservative	0; Mismatches 102; Indels 4; Gaps 2;
QY	47 CCGTCATGATGCTCTATCAGAGCAATGGCATTGTCATTAAACCTTTGAAAAGC 106
Db	230 CCATCATGATGTTCTCCAGAGCAAAATGGCACCTTGGCTTAAACCTTTGAAAACGC 289
QY	107 TAGGGGAAAAACAACCTCAACAACTATTATTTTTC-CCCATGAGCATATCATCGCCTTGG 165
Db	290 TGGGTAAGACAACTCGAAGATGTTTCTTCTACCCATGAGCATGCTGTGCTCCCTGG 349
QY	166 CCATCGTTTTCATGGGGGCAAGGAAACACTGCAGCTCAGATGCTCTCAGCGCACTTTGTT 225
Db	350 CCATGCTCTACATGGGGGCAAGGAAACACCGCTGCACAGATGCCCGCCAGATACCTTCTT 409
QY	226 TTAGTAAATCGAGGTGAAGATCGAGATATTATTCAGAGTCTTTTCAGTCACTTCTTTGTTG 285
Db	410 TCAATAAAGTGGCGT---GGTGGAGACATCCACAGGGCTTCAGATCTCTTCTACCG 466
QY	286 CAATTAAACGAACACTGACACTGAATATGCTTTAGAACTGCCAACGGGCTCTTTGGAGAAA 345
Db	467 AAGTGAACAAAGACTGGCAGCAGTACTTGCCTTAGGGTGGCCAAAGGCTCTTTGGGAAA 526
QY	346 AGCTTTATGATTTCTCTCACAGGTTTACAGATTTCTGTGGCAATTTTACCAAGCAAGA 405
Db	527 AGCTCTTGATTTCTCTCTCATCTTTAGAGATTTCTGCAAAAATTTTACCAAGCAGAGA 586
QY	406 TAAACACAGTACACTTTTGTGAATATACAGAGAAAGTCCACACACGCTGTAACCTCCTGG 465
Db	587 TGGAGGAGCTTGACTTTATCAGCGCGGTAGAGAGTCCAGAAACACATATAACACCTGG 646
QY	466 TTGCTGATAAACTAAAG 483
Db	647 TAGCTGAAAAGACAGAGAAG 664
RESULT 13	
AK094983	
LOCUS	AK094983.1 GI:21754158
DEFINITION	Homo sapiens CDNA FLJ37664 fis, clone BRHIP2011491, highly similar to PLACENTAL THROMBIN INHIBITOR.
ACCESSION	AK094983
VERSION	AK094983.1
KEYWORDS	oligo capping; fis (full insert sequence).
SOURCE	Homo sapiens hippocampus CDNA to mRNA, clone BRHIP2011491.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuno, Y., Nagai, K. and Isogai, T.
TITLE	NEDO human cDNA sequencing project
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 2036)
AUTHORS	Isogai, T. and Yamamoto, J.
TITLE	Direct Submission
JOURNAL	Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamata, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp , Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library construction: Helix Research Institute (HRI); CDNA library Key Technology Center etc.; 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
FEATURES	Location/Qualifiers 1..2036 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="BRHIP2011491" /tissue_type="hippocampus" /clone_lib="BRHIP2" /note="cloning vector: pME18SFLJ"
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		/clone="SPLEN2000247"
		/tissue type="spleen"
		/clone_lib="SPLEN2"
		/notes="cloning vector: pME18SFL3"
BASE COUNT	796 a 828 c 799 g 848 t	
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Query Match	35.0%; Score 246.8; DB 9; Length 3271;	
Best Local Similarity	75.8%; Pred. No. 9.2e-60;	
Matches	332; Conservative 0; Mismatches 102; Indels 4; Gaps 2;	
QY	47	CCGTCATGATGCTCTATCAGAGCAAAATGGACATTTGGCATTAACCTTTTGAAGAAGC 106
Db	774	CCATCATGATGCTTCGCGAGAGCAAAATGGACATTTGGCATTAACCTTTTGAAGAAGC 833
QY	107	TAGGGGAAACCACTCAAACTTATTTTTC-CCCATGAGCATATCATCAGCCTTGG 165
Db	834	TGGTAAAGCAACTCGAAGATGCTTTTTCACCCATGAGCATGCTTGTGCTGCTGG 893
QY	166	CCATGCTTTTTCATGGGGCAAGGAAACACTGCGAGCTCAGATGCTCAGGCATTTGTT 225
Db	894	CCATGCTTACATGGGGCAAGGAAACACTGCGAGCTCAGATGCTCAGGCATTTGTT 953
QY	226	TTAGTAAATCGAGGTGAAGATGAGATATTCATCGAGGTTTTCAGTCACCTTTGTTG 285
Db	954	TCATTAATGAGTGGCGT---GGTGGAGACATCCACAGGGCTTCAGTCTTCTCACCG 1010
QY	286	CAATTAAACGAACCTGACACTGAATATGCTTTAGAACTGCCAACCGGCTTTTGGAGAA 345
Db	1011	AGTGAACAGACTGCGACGCACTACTTCTTAGGATGGCCAAACAGGCTCTTTGGGAAA 1070
QY	346	AGTCTTATGATTTCTTCAGAGTTTACAGATTCCTGTGGCAATTTTACCAAGCAAGA 405
Db	1071	AGTCTTGTGATTTCTCTCATCTTTTATGAGATTCCTGCCAAATTTTACCAAGCAGA 1130
QY	406	TAAACAGCTAGACTTTGTGAATGATACAGAGAAAGTCCCAACACGCTGTAAACTCCTGG 465
Db	1131	TGAGAGAGCTTGACTTTTATCAGCGCGTAGAGAGTCCAGAAACACATAAACACCTGG 1190
QY	466	TTGCTGATAAACTAAAG 483
Db	1191	TAGCTGAAAGACAGAGAAG 1208

RESULT 15
AK057138
LOCUS
DEFINITION
Homo sapiens cDNA FLJ23576 fis, clone SPLEN2000247, highly similar to PLACENTAL THROMBIN INHIBITOR.
ACCESSION
AK057138.1 GI:16552727.
VERSION
oligo capping; fis (full insert sequence).
KEYWORDS
Homo sapiens spleen cDNA to mRNA, clone_lib:SPLEN2
SOURCE
clone:SPLEN2000247.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Kawakami,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Suzuki,Y., Sugano,S., Nagahara,K., Maehori,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
Unpublished
TITLE
NEDO human cDNA sequencing project
JOURNAL
REFERENCE
2 (bases 1 to 3271)
AUTHORS
Isogai,T., Otsuki,T. and Sugiyama,T.
TITLE
Direct Submission
JOURNAL
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and

QY	47	CCGTCATGATGCTCTATCAGAGCAAAATGGACATTTGGCATTAACCTTTTGAAGAAGC 106
Db	774	CCATCATGATGCTTCGCGAGAGCAAAATGGACATTTGGCATTAACCTTTTGAAGAAGC 833
QY	107	TAGGGGAAACCACTCAAACTTATTTTTC-CCCATGAGCATATCATCAGCCTTGG 165
Db	834	TGGTAAAGCAACTCGAAGATGCTTTTTCACCCATGAGCATGCTTGTGCTGCTGG 893
QY	166	CCATGCTTTTTCATGGGGCAAGGAAACACTGCGAGCTCAGATGCTCAGGCATTTGTT 225
Db	894	CCATGCTTACATGGGGCAAGGAAACACTGCGAGCTCAGATGCTCAGGCATTTGTT 953
QY	226	TTAGTAAATCGAGGTGAAGATGAGATATTCATCGAGGTTTTCAGTCACCTTTGTTG 285
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QY	286	CAATTAAACGAACCTGACACTGAATATGCTTTAGAACTGCCAACCGGCTTTTGGAGAA 345
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QY	346	AGTCTTATGATTTCTTCAGAGTTTACAGATTCCTGTGGCAATTTTACCAAGCAAGA 405
Db	1071	AGTCTTGTGATTTCTCTCATCTTTTATGAGATTCCTGCCAAATTTTACCAAGCAGA 1130
QY	406	TAAACAGCTAGACTTTGTGAATGATACAGAGAAAGTCCCAACACGCTGTAAACTCCTGG 465
Db	1131	TGAGAGAGCTTGACTTTTATCAGCGCGTAGAGAGTCCAGAAACACATAAACACCTGG 1190
QY	466	TTGCTGATAAACTAAAG 483
Db	1191	TAGCTGAAAGACAGAGAAG 1208
RESULT 15		
AK057138		
LOCUS		
DEFINITION		
Homo sapiens cDNA FLJ23576 fis, clone SPLEN2000247, highly similar to PLACENTAL THROMBIN INHIBITOR.		
ACCESSION		
AK057138.1		
VERSION		
oligo capping; fis (full insert sequence).		
KEYWORDS		
Homo sapiens spleen cDNA to mRNA, clone_lib:SPLEN2		
SOURCE		
clone:SPLEN2000247.		
ORGANISM		
Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE		
1		
AUTHORS		
Kawakami,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Suzuki,Y., Sugano,S., Nagahara,K., Maehori,Y., Nagai,K. and Isogai,T.		
NEDO human cDNA sequencing project		
Unpublished		
TITLE		
NEDO human cDNA sequencing project		
JOURNAL		
REFERENCE		
2 (bases 1 to 3271)		
AUTHORS		
Isogai,T., Otsuki,T. and Sugiyama,T.		
TITLE		
Direct Submission		
JOURNAL		
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)		
COMMENT		
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and		

AK027149 2759 bp mRNA linear PRI 29-SEP-2000
Homo sapiens cDNA: FLJ23496 fis, clone LNG02535, highly similar to S69272 human mRNA for cytoplasmic antiproteinase-38 kDa intracellular serine proteinase inhibitor.
AK027149
ACCESSION
AK027149.1 GI:10440203
VERSION
oligo capping; fis (full insert sequence).
KEYWORDS
Homo sapiens human lung cDNA to mRNA, clone_lib:LNG
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2759)
AUTHORS
Kawakami,T., Noguchi,S., Itch,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
TITLE
NEDO human cDNA sequencing project
JOURNAL
REFERENCE
2 (bases 1 to 2759)
AUTHORS
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,

Shibahara, T., Tanaka, T. and Nakamura, Y.
 Direct Submission
 Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
 University of Tokyo, Laboratory of Genome Structure Analysis, Human
 Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
 Japan (E-mail: cdnal@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,
 Fax: 81-3-5449-5416)
 NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; cDNA full insert
 sequencing: Research Association for Biotechnology; cDNA library
 construction, 5'- & 3'-end one pass sequencing: Department of
 Virology and Human Genome Center, Institute of Medical Science,
 University of Tokyo (partly supported by Science and Technology
 Agency).

FEATURES

source

Location/Qualifiers

1..2759
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="LNG02535"
 /tissue_type="human lung"
 /clone_lib="LNG"
 /note="cloning vector pME18SFL3"

misc_feature

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 /note="highly similar to S69272 human mRNA for cytoplasmic
 antiproteinase-38 kda intracellular serine proteinase
 inhibitor"

BASE COUNT 682 a 709 c 681 g 687 t
 ORIGIN

Query Match

Best Local Similarity 34.7%; Score 245.2; DB 9; Length 2759;

Matches 331; Conservative 0; Mismatches 103; Indels 4; Gaps 2;

QY 47 CCGTCATGGATGCTCTATCAGAACAAATGGCACATTGGCATTAAACCTTTGAAAAAGC 106
 Db |||||
 QY 1465 CCATCATGGATGTTCTCGCAGAGCAATGGCACCTTTGCTTAAACCTTTGAAAAACAC 1524
 Db |||||
 QY 107 TAGGGGAAAAACACTCAAAACCTTATTTTTC-CCCATGAGCATATCATCAGCCTGG 165
 Db |||||
 QY 1525 TGGGTAAAGACAACTCGAGATGTGTTTTCTACCCCATGAGCATGCTGTGCCCTGG 1584
 Db |||||
 QY 166 CCATGGTTTTCATGGGGGCAAGGAAACACTGCAGCTCAGATGCTCAGGCACCTTTGT 225
 Db |||||
 QY 1585 CCATGGTCTACATGGGGGCAAGGAAACACCCTGCACAGATGGCCGAGATCTTTCT 1644
 Db |||||
 QY 226 TTAGTAAATCGGAGTGAGATGGAGATATTCATCGAGTTTTCAGTCACCTTTGTGTTG 285
 Db |||||
 QY 1645 TCAATAAAGTGCGGT--GGTGGAGACATCCACAGGGCTTCCAGTCTCTCTCACCG 1701
 Db |||||
 QY 286 CAATTAAACAGAACTGACACTGAATATGTGCTTAGAACTGCCAACGGCTCTTTGGAGAA 345
 Db |||||
 QY 1702 AAGTGAACAAGACTGGCAGCAGTACTTGTAGGATGCCAACAGGCTCTTTGGGGAAA 1761
 Db |||||
 QY 346 AGCTTTATGATTTCCCTCAGAGTTTACAGATTCTGTGGCAAAATTTACCAAGCAACGA 405
 Db |||||
 QY 1762 AGTCTGTGATTTCTCTCATCTTTTAGAGATTCTCTGCCAAAAATTTACCAAGCGGAGA 1821
 Db |||||
 QY 406 TAAACAGCTTAGACTTTTGTGAATGATACAGAGAAGTCCACACAGTGTAAACTCTGGG 465
 Db |||||
 QY 1822 TGGAGGAGCTTGACTTTATCAGCGCGGTAGAGAGTCCAGAAAAACACATAAACACCTGGG 1881
 Db |||||
 QY 466 TTCTGATAAACTAAAG 483
 Db |||||
 QY 1882 TAGCTGAAAAGACAGAAAG 1899
 Db |||||

Search completed: May 21, 2003, 17:33:27
 Job time : 2178 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	704	99.7	706	21	AAAG4690
2	704	99.7	706	23	AAAL42746
3	586	83.0	599	21	AAAT4934
4	586	83.0	599	23	AAAL42747
5	577	81.7	608	21	AAAT4935
6	577	81.7	608	23	AAAL42748
7	462.8	65.6	943	24	ABK94967
8	251.2	35.6	1624	21	AAF16065
9	250.4	35.5	695	22	AA506075

29-FEB-2000; 2000WO-US05082.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

XX 01-MAR-1999; 99US-0122276.
PR 12-MAR-1999; 99US-0124094.
PR 18-AUG-1999; 99US-0149452.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Ni J;
PI WPI; 2000-579284/54.
DR P-PSDB; AAB08776.
XX Novel human serine protease inhibitor superfamily of proteins useful
PT for diagnosing, treating, preventing and/or prognosing disorders
PT related to the serpin polypeptides
XX Claim 1; Page 202; 215pp; English.
XX The present sequence encodes a human serpin polypeptide. Serpin is
CC a member of the serine protease inhibitor superfamily of polypeptides.
CC The serpin polynucleotides and polypeptides are used to prevent, treat
CC or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
CC horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiodysplasia, nervous system disorders,
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. The polypeptides can
CC also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities.
XX Query Match 99.7%; Score 704; DB 21; Length 706;
XX Best Local Similarity 100.0%; Pred. NO. 8.3e-199; Indels 0; Gaps 0;
XX Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCACGAGCTTCGCTCTGGGACGCTGGGGGAGAACTGGGGCTCAACGCTCATGGATGCT 60
DB 1 GGCACGAGCTTCGCTCTGGGACGCTGGGGGAGAACTGGGGCTCAACGCTCATGGATGCT 60
QY 61 CTATCAGAAGCAATGGCAGATTTGGCAATTAACCTTTTGAAGAGCTAGGGAAACAC 120
DB 61 CTATCAGAAGCAATGGCAGATTTGGCAATTAACCTTTTGAAGAGCTAGGGAAACAC 120
QY 121 TCMAACAACTTATTTTTCCTCCATGAGCATATCATCAGCTTGGCCATGTTTTCATGG 180
DB 121 TCMAACAACTTATTTTTCCTCCATGAGCATATCATCAGCTTGGCCATGTTTTCATGG 180
QY 181 GGGCAAGGAGAAACACATCGAGTCATGCTCAGGCACTTTGTTAGTAAATCGGAG 240
DB 181 GGGCAAGGAGAAACACATCGAGTCATGCTCAGGCACTTTGTTAGTAAATCGGAG 240
QY 241 GTGAAGATGGAGATTTTCATCGAGTTTTCAGTCACTTCTGTTGCAATTAACAGAACTG 300
DB 241 GTGAAGATGGAGATTTTCATCGAGTTTTCAGTCACTTCTGTTGCAATTAACAGAACTG 300
QY 301 ACACCTGAATATGCTGTAGAACTGCCAACGGGCTTTTGGAGAAAGCTTTATGATTTCC 360
DB 301 ACACCTGAATATGCTGTAGAACTGCCAACGGGCTTTTGGAGAAAGCTTTATGATTTCC 360
QY 361 TCACAGGTTTTCAGATTTCTGTCGAATTTCTACCAAGCAACGATTAACAGCTAGACT 420
DB 361 TCACAGGTTTTCAGATTTCTGTCGAATTTCTACCAAGCAACGATTAACAGCTAGACT 420
QY 421 TTGTGAATCATACAGAGAGTCCACACACGCTGTAAACTCCTGGGTTGCTGATAAACTA 480
DB 421 TTGTGAATCATACAGAGAGTCCACACACGCTGTAAACTCCTGGGTTGCTGATAAACTA 480

QY 481 AGCCTGGAAATTTATTCAACAAAGCCTGTACATCTGAGGAGCCAGGAATCGCCTCTT 540
DB 481 AGCCTGGAAATTTATTCAACAAAGCCTGTACATCTGAGGAGCCAGGAATCGCCTCTT 540
QY 541 CCTCTTTTACTGCAAAAGCCTGCTTTTCACAGCCCTACTGTTTCTATTTCCCAAT 600
DB 541 CCTCTTTTACTGCAAAAGCCTGCTTTTCACAGCCCTACTGTTTCTATTTCCCAAT 600
QY 601 GCAACTCTCTGACCCCGCATGGCATGTGTGNGCTCCCTCCCTGTGAGCAGNTGTGA 660
DB 601 GCAACTCTCTGACCCCGCATGGCATGTGTGNGCTCCCTCCCTGTGAGCAGNTGTGA 660
QY 661 CTAAATAACTGCGCCCAATTTTCATCTGTAAATAAAAAAAAAAAAAA 706
DB 661 CTAAATAACTGCGCCCAATTTTCATCTGTAAATAAAAAAAAAAAAAA 706
RESULT 2
AAL42746
ID AAL42746 standard; cDNA; 706 BP.
XX AAL42746;
AC AAL42746;
XX 19-JUL-2002 (first entry)
DT Human serine protease inhibitor (serpin) coding sequence HMC1S41.
XX Human; serine protease inhibitors; serpin; blood coagulation;
KW proteinase-activated physiological process; gene therapy;
KW antitense therapy; cancer; inflammation; neurological disease;
KW immune disease; gene; ss; HMC1S41.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 3..650
FT /*tag= a
FT /partial
FT /product= "Human serpin protein HMC1S41"
FT /transl_except= (pos:632..635, aa:Xaa)
FT /note= "No start codon is given; Xaa is unknown"
XX - WO200155390-A1.
PN 02-AUG-2001.
XX 26-JAN-2001; 2001WO-US02484.
XX 28-JAN-2000; 2000US-0178769.
XX 29-FEB-2000; 2000WO-US05082.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ni J, Ruben SM, Shi Y;
XX WPI; 2001-457730/49.
XX P-PSDB; AAO14914.
XX Isolated serine protease inhibitor polypeptide for treating, preventing
PT and/or prognosing cancers, inflammation, immune disorders and
PT neurological diseases and also for testing and detection e.g. diagnosis
PT -
XX Claim 1; Page 273; 288pp; English.
XX The invention comprises the amino acid and coding sequences of a group of
CC novel human serine protease inhibitors (serpins). Serpins are a
CC superfamily of single chain proteins that contain a conserved structure
CC of approximately 370-420 amino acids and generally range between 50 and
CC 100 kDa in molecular mass. The majority of serpins function as protease
CC inhibitors and so are involved in the regulation of several proteinase-
CC activated physiological processes (e.g. blood coagulation). The Serpin

CC DNA and amino acid sequences of the invention are useful in the treatment
 CC (e.g. gene therapy, antisense therapy) and diagnosis of conditions such
 CC as cancer, inflammation, neurological diseases and immune diseases. The
 CC present cDNA sequence represents a human serpin coding sequence of the
 CC invention.
 XX
 SQ Sequence 706 BP; 207 A; 166 C; 148 G; 183 T; 2 other;

Query Match 99.7%; Score 704; DB 23; Length 706;
 Best Local Similarity 100.0%; Pred. No. 8.3e-199;
 Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCACGAGCTTCCTCTCGGAGCTGCGCGGAGAACTGGGGCTACCGCTATGATGCT 60
 Db 1 GGCACGAGCTTCCTCTCGGAGCTGCGCGGAGAACTGGGGCTACCGCTATGATGCT 60
 Qy 61 CTATCAGAACAAATGGCACAATTTGCATTAAACCTTTTGAAGAAGCTAGGGAAACAC 120
 Db 61 CTATCAGAACAAATGGCACAATTTGCATTAAACCTTTTGAAGAAGCTAGGGAAACAC 120
 Qy 121 TCAACAACTTATTTTCCCATGAGCATATCATCAGCTTGGCCATGGTTTTCATGG 180
 Db 121 TCAACAACTTATTTTCCCATGAGCATATCATCAGCTTGGCCATGGTTTTCATGG 180
 Qy 181 GGGCAAGGGAACACTGCGAGCTCAGATGCTCAGCAGCACTTTGTTAGTAAATCGGAG 240
 Db 181 GGGCAAGGGAACACTGCGAGCTCAGATGCTCAGCAGCACTTTGTTAGTAAATCGGAG 240
 Qy 241 GTGAAGATGAGATATTTATCATGAGGTTTTCAGTCACTTCTTGTGCAATTAACAGAACTG 300
 Db 241 GTGAAGATGAGATATTTATCATGAGGTTTTCAGTCACTTCTTGTGCAATTAACAGAACTG 300
 Qy 301 ACACCTGAATATGCTTGAAGCTGCAAGGGCTTTTGGAGAAAGTCTTATGATTTCC 360
 Db 301 ACACCTGAATATGCTTGAAGCTGCAAGGGCTTTTGGAGAAAGTCTTATGATTTCC 360
 Qy 361 TCACAGGTTTACAGATTCCTGCGCAATTTCTACCAAGCAAGATTAACAGAGTAGACT 420
 Db 361 TCACAGGTTTACAGATTCCTGCGCAATTTCTACCAAGCAAGATTAACAGAGTAGACT 420
 Qy 421 TTGTGAATGATACAGAGAAGTCCACACAGCTGTAACCTCCTGGGTTGCTGATAAACTA 480
 Db 421 TTGTGAATGATACAGAGAAGTCCACACAGCTGTAACCTCCTGGGTTGCTGATAAACTA 480
 Qy 481 AAGCCTGGAATATTTCAACAAGCCTGTCATCTGAGGAGCCAGGAATCGCTCTT 540
 Db 481 AAGCCTGGAATATTTCAACAAGCCTGTCATCTGAGGAGCCAGGAATCGCTCTT 540
 Qy 541 CCTCTGTTACTGCAAGCCTGCTTTCACAGCCCTACTGCTTCACTCTATTTCCCAAT 600
 Db 541 CCTCTGTTACTGCAAGCCTGCTTTCACAGCCCTACTGCTTCACTCTATTTCCCAAT 600
 Qy 601 GCAACTCTCTGTGACCCCGCATGATGCTGTCGTCCTCCCTGCTGAGCAGNTGTA 660
 Db 601 GCAACTCTCTGTGACCCCGCATGATGCTGTCGTCCTCCCTGCTGAGCAGNTGTA 660
 Qy 661 CTAATAAATCGCGCAATTTTCATCTGTAATAAAAAAAAAAAAAA 706
 Db 661 CTAATAAATCGCGCAATTTTCATCTGTAATAAAAAAAAAAAAAA 706

RESULT 3
 ID AAA74934
 XX AAA74934 standard; DNA; 599 BP.
 AC AAA74934;
 XX
 DT 02-JAN-2001 (first entry)
 DE Nucleotide sequence encoding a human serpin polypeptide.
 XX Human; serpin; serine protease inhibitor; autoimmune disease; neoplasm;
 KW rheumatoid arthritis; hyperproliferative disorder; cerebral ischemia;

KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;
 KW ocular disorder; corneal infection; epithelial cell proliferation;
 KW skin aging; sunburn; wound healing; organ transplantation; chemotaxis;
 KW food additive; food preservative; ss.
 XX Homo sapiens.
 XX OS
 FH Key Location/Qualifiers
 FT CDS 1..597
 FT /tag= a
 FT /transl_except= (pos: 583..585, aa: Xaa)
 FT /product= "serpin"
 FT /note= "Xaa is any L-amino acid; no termination codon
 given"

WO200052160-A1.
 08-SEP-2000.
 29-FEB-2000; 2000WO-US05082.
 01-MAR-1999; 99US-0122276.
 12-MAR-1999; 99US-0124094.
 18-AUG-1999; 99US-0149452.
 (HUMA-) HUMAN GENOME SCI INC.
 Ruben SM, Ni J;
 WPI; 2000-579284/54.
 P-PSDB; AAB08783.
 Novel human serine protease inhibitor superfamily of proteins useful
 for diagnosing, treating, preventing and/or prognosing disorders
 related to the Serpin polypeptides -
 Claim 1; Page 12-13; 215pp; English.

The present sequence encodes a human serpin polypeptide. Serpin is
 a member of the serine protease inhibitor superfamily of polypeptides.
 The serpin polynucleotides and polypeptides are used to prevent, treat
 or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
 horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
 treated include autoimmune diseases e.g. rheumatoid arthritis
 hyperproliferative disorders e.g. neoplasms of the breast or liver,
 cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 e.g. cerebral ischemia, angiogenesis, nervous system disorders,
 e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 fungi and ocular disorders e.g. corneal infection. The polypeptides can
 also be used to aid wound healing and epithelial cell proliferation,
 to prevent skin aging due to sunburn, to maintain organs before
 transplantation, for supporting cell culture of primary tissues, to
 regenerate tissues and in chemotaxis. The polypeptides can also be used
 as a food additive or preservative to increase or decrease storage
 capabilities.

Sequence 599 BP; 171 A; 141 C; 122 G; 164 T; 1 other;
 Query Match 83.0%; Score 586; DB 21; Length 599;
 Best Local Similarity 99.8%; Pred. No. 8.7e-164;
 Matches 598; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 52 ATGGATGCTCTATCAGAGCAATGGCACAATTTGCAATTAACCTTTTGAAGAAGCTAGGG 111
 Db 1 ATGGATGCTCTATCAGAGCAATGGCACAATTTGCAATTAACCTTTTGAAGAAGCTAGGG 60
 Qy 112 GAAACAACTCAAACTTATTTTTCATGAGCATATCATCAGCTTGGCCATG 170
 Db 61 GAAACAACTCAAACTTATTTTTCATGAGCATATCATCAGCTTGGCCATG 120
 Qy 171 GTTTTCATGGGCAAGGGAACACTGAGCTCAGATGCTCAGGCACTTTTGTAGT 230

Db	121	GT	TTT	CAT	GGGG	CAAA	GGGAA	CACT	CGAG	TG	CT	CAG	AT	GT	CT	CAG	CA	CT	TT	GT	T	AG	T	180
Qy	231	AAA	AT	CGG	AGG	TGA	GAT	AT	T	CAT	CG	AG	T	T	T	T	T	T	T	T	T	T	T	290
Db	181	AAA	AT	CGG	AGG	TGA	GAT	AT	T	CAT	CG	AG	T	T	T	T	T	T	T	T	T	T	T	240
Qy	291	AA	CAGA	AAC	TG	CA	CT	GA	AT	T	G	T	T	T	T	T	T	T	T	T	T	T	T	350
Db	241	AA	CAGA	AAC	TG	CA	CT	GA	AT	T	G	T	T	T	T	T	T	T	T	T	T	T	T	300
Qy	351	TAT	GAT	T	T	C	T	CAC	AG	T	T	T	T	T	T	T	T	T	T	T	T	T	T	410
Db	301	TAT	GAT	T	T	C	T	CAC	AG	T	T	T	T	T	T	T	T	T	T	T	T	T	T	360
Qy	411	CAC	G	T	A	G	A	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	470
Db	361	CAC	G	T	A	G	A	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	420
Qy	471	GAT	AAA	AAC	TAA	AGC	CTG	GA	AA	A	T	T	T	T	T	T	T	T	T	T	T	T	T	530
Db	421	GAT	AAA	AAC	TAA	AGC	CTG	GA	AA	A	T	T	T	T	T	T	T	T	T	T	T	T	T	480
Qy	531	AT	CGC	T	C	T	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	590
Db	481	AT	CGC	T	C	T	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	540
Qy	591	ATT	CCC	AAA	TG	CA	AC	T	CT	C	T	C	T	GT	GA	CC	CG	CA	TG	GC	AT	GT	GC	649
Db	541	ATT	CCC	AAA	TG	CA	AC	T	CT	C	T	C	T	GT	GA	CC	CG	CA	TG	GC	AT	GT	GC	599

RESULT 4	
AAAL42747	
ID	AAAL42747 standard; cDNA; 599 BP.
XX	
XX	AAAL42747;
XX	
XX	19-JUL-2002 (first entry)
XX	
XX	Human serine protease inhibitor (serpin) coding sequence 1.
DE	
XX	Human; serine protease inhibitors; serpin; blood coagulation;
KW	proteinase-activated physiological process; gene therapy;
KW	antitense therapy; cancer; inflammation; neurological disease;
KW	immune disease; gene; ss.
XX	
OS	Homo sapiens.
XX	
XX	
Key	Location/Qualifiers
FT	1..597
FT	/*tag= a
FT	/product= "Human serpin protein 1"
FT	/transl except= (pos:583..585, aa:Xaa)
FT	/note= "Xaa is unknown"
XX	
XX	
PN	WO200155390-A1..
XX	
PD	02-AUG-2001.
XX	
XX	
PF	26-JAN-2001; 2001WO-US02484.
XX	
XX	
PR	28-JAN-2000; 2000US-0178769.
PR	29-FEB-2000; 2000WO-US05082.
XX	
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Ni J, Ruben SM, Shi Y;
XX	
XX	
WPI	2001-457730/49.
DR	P-PSDB; AAOL4921.
DR	
XX	
XX	
PT	Isolated serine protease inhibitor polypeptide for treating, preventing
PT	and/or procuring cancers, inflammation, immune disorders and

neurological diseases and also for testing and detection e.g. diagnosis

Claim 1; Page 14-15; 288pp; English.

The invention comprises the amino acid and coding sequences of a group of novel human serine protease inhibitors (serpins). Serpins are a superfamily of single chain proteins that contain a conserved structure of approximately 370-420 amino acids and generally range between 50 and 100 kDa in molecular mass. The majority of serpins function as protease inhibitors and so are involved in the regulation of several proteinase-activated physiological processes (e.g. blood coagulation). The Serpin DNA and amino acid sequences of the invention are useful in the treatment (e.g. gene therapy, antisense therapy) and diagnosis of conditions such as cancer, inflammation, neurological diseases and immune diseases. The present cDNA sequence represents a human serpin coding sequence of the invention.

Sequence 599 BP; 171 A; 141 C; 122 G; 164 T; 1 other;

Query Match 83.0%; Score 586; DB 23; Length 599;
 Best Local Similarity 99.8%; Pred. No. 8.7e-164;
 Matches 598; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 52 ATGGATGCTCTATCAGAAGCAAAATGGCACATTTGTCATTAACCTTTTGAAGAAAGCTAGGG 111
 DB 1 ATGGATGCTCTATCAGAAGCAAAATGGCACATTTGTCATTAACCTTTTGAAGAAAGCTAGGG 60

QY 112 GAAAAACACTCAAAACACTTATTTTTT-CCCATGAGCATATCATCAGCCTTGGCCCATG 170
 DB 61 GAAAAACACTCAAAACACTTATTTTTTCCCATGAGCATATCATCAGCCTTGGCCCATG 120

QY 171 GTTTTCATGGGGCAAGGGAACACATCGAGCTCAGATGTCTCAGGCACCTTGTGTTTAGT 230
 DB 121 GTTTTCATGGGGCAAGGGAACACATCGAGCTCAGATGTCTCAGGCACCTTGTGTTTAGT 180

QY 231 AAAATCGGAGGTGAAGATGGAGATATTCATCGAGGTTTTTCAGTCACCTTCTTGTTGCAATT 290
 DB 181 AAAATCGGAGGTGAAGATGGAGATATTCATCGAGGTTTTTCAGTCACCTTCTTGTTGCAATT 240

QY 291 AACGAACTGCACACTGAAATATGTCTAGAACTGCCAACGGGCTCTTTGGAGAAAAGTCT 350
 DB 241 AACGAACTGCACACTGAAATATGTCTAGAACTGCCAACGGGCTCTTTGGAGAAAAGTCT 300

QY 351 TATGATTTCTCTCACAGGTTTTTACAGATTCCTGTGGCAAAATTTCTACCAAGCAACGATAAAA 410
 DB 301 TATGATTTCTCTCACAGGTTTTTACAGATTCCTGTGGCAAAATTTCTACCAAGCAACGATAAAA 360

QY 411 CAGCTAGACTTTGTGAATGATACAGAGAAGTCCACACACAGCTGTAAACTCCTCGGTTGCT 470
 DB 361 CAGCTAGACTTTGTGAATGATACAGAGAAGTCCACACACAGCTGTAAACTCCTCGGTTGCT 420

QY 471 GATAAACTAAAGCCTGGAAAATTTATTTCAAAACAGCCTGTCCACATCTGGAGAGCCAGGA 530
 DB 421 GATAAACTAAAGCCTGGAAAATTTATTTCAAAACAGCCTGTCCACATCTGGAGAGCCAGGA 480

QY 531 ATCGCCTCTTTCCTTTGTTACTGCAAAAGCCTGCTTTTCA CAGGCCCTACTCGTTCACTCT 590
 DB 481 ATCGCCTCTTTCCTTTGTTACTGCAAAAGCCTGCTTTT CACAGGCCCTACTCGTTCACTCT 540

QY 591 ATTCCTCAAAATGCAACTCTCTCGTCACCCCGCATGGCATGTGGTGNCTCCCTCCCTCTGTG 649
 DB 541 ATTCCTCAAAATGCAACTCTCTCGTCACCCCGCATGGCATGTGGTGNCTCCCTCCCTCTGTG 599

RESULT 5
 AAA74935
 ID AAA74935 standard; DNA; 608 BP.
 XX
 AC AAA74935;
 XX
 DT 02-JAN-2001 (first entry)
 XX

DE Nucleotide sequence encoding a human serpin polypeptide.

XX Human; serpin; serine protease inhibitor; autoimmune disease; neoplasm;
 KW rheumatoid arthritis; hyperproliferative disorder; cerebral ischemia;
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;
 KW ocular disorder; corneal infection; epithelial cell proliferation;
 KW skin aging; sunburn; wound healing; organ transplantation; chemotaxis;
 KW food additive; food preservative; ss.

XX Homo sapiens.

OS Key Location/Qualifiers
 XX CDS 1..606
 FT /*tag= a
 FT /transl_except= (pos: 91..93, aa: Xaa)
 FT /transl_except= (pos: 94..96, aa: Xaa)
 FT /transl_except= (pos: 97..99, aa: Xaa)
 FT /product= "serpin"
 FT /note= "Xaa is any L-amino acid; no termination codon given"

XX WO200052160-A1.
 XX 08-SEP-2000.
 XX 29-FEB-2000; 2000WO-US05082.
 XX 01-MAR-1999; 99US-0122276.
 XX 12-MAR-1999; 99US-0124094.
 XX 18-AUG-1999; 99US-0149452.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Ni J;
 XX WPI; 2000-579284/54.
 XX P-PSDB; AAB08784.

PT Novel human serine protease inhibitor superfamily of proteins useful
 PT for diagnosing, treating, preventing and/or prognosing disorders
 PT related to the Serpin polypeptides

XX Claim 1; Page 13; 215pp; English.

CC The present sequence encodes a human serpin polypeptide. Serpin is
 CC a member of the serine protease inhibitor superfamily of polypeptides.
 CC The serpin polynucleotides and polypeptides are used to prevent, treat
 CC or ameliorate a medical conditions in e.g. humans, mice, rabbits, goats,
 CC horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
 CC treated include autoimmune diseases e.g. rheumatoid arthritis,
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 CC e.g. cerebral ischemia, angioneurosis, nervous system disorders.
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 CC fungi and ocular disorders e.g. corneal infection. The polypeptides can
 CC also be used to aid wound healing and epithelial cell proliferation,
 CC to prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, for supporting cell culture of primary tissues, to
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used
 CC as a food additive or preservative to increase or decrease storage
 CC capabilities.

XX Sequence 608 BP; 171 A; 141 C; 122 G; 164 T; 10 other;
 SQ

Query Match 81.7%; Score 577; DB 21; Length 608;
 Best Local Similarity 98.4%; Pred. No. 4.1e-161;
 Matches 598; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 52 ATGGATGCTCTATCAGAGCAATGGACATTTGCATTAAACCTTTTGAAGAGCTAGGG 111
 DB 1 ATGGATGCTCTATCAGAGCAATGGACATTTGCATTAAACCTTTTGAAGAGCTAGGG 60

QY 112 GAAGCAACTCAACAACTTATTTTTC-----CCATGAGCATATCATCAGCC 161
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 GAAACAACTCAACAACTTATTTTTCNNNNNNNNNNCCATGAGCATATCATCAGCC 120
 QY 162 TTGGCCATGGTTTTCATGGGGCAAGGAAACACTGCGAGCTCAGATGCTCAGGCACTT 221
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
 121 TTGGCCATGGTTTTCATGGGGCAAGGAAACACTGCGAGCTCAGATGCTCAGGCACTT 180
 QY 222 TGTTTTAGTAAATCGGAGGTGAAGATGGAGATATTCATCGAGGTTTTCAGTCACTTCTT 281
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
 181 TGTTTTAGTAAATCGGAGGTGAAGATGGAGATATTCATCGAGGTTTTCAGTCACTTCTT 240
 QY 282 GTTGCAATTAACAGAACTGACACTGAATATGCTTAGAACTGCCAAGGCTCTTTTGA 341
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
 241 GTTGCAATTAACAGAACTGACACTGAATATGCTTAGAACTGCCAAGGCTCTTTTGA 300
 QY 342 GAAAGTCTTATGATTTTCTCACAGGTTTACAGATTCCTGTGGCAATTTCTACCAAGCA 401
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
 301 GAAAGTCTTATGATTTTCTCACAGGTTTACAGATTCCTGTGGCAATTTCTACCAAGCA 360
 QY 402 ACGATAAACAGCTAGACTTTTGTGAATGATACAGAGAGTCCACACGCTGTAACCTCC 461
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
 361 ACGATAAACAGCTAGACTTTTGTGAATGATACAGAGAGTCCACACGCTGTAACCTCC 420
 QY 462 TGGGTTGCTGATAAACTAAAGCCTGGAATAATTTTCAAAACAGCCTGTACATCTGGAG 521
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
 421 TGGGTTGCTGATAAACTAAAGCCTGGAATAATTTTCAAAACAGCCTGTACATCTGGAG 480
 QY 522 GAGCCAGGAATCGGCTCTTCTCTTGTACTGCAAGCCTGCGCTTTCACAGCCCTACTG 581
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
 481 GAGCCAGGAATCGGCTCTTCTCTTGTACTGCAAGCCTGCGCTTTCACAGCCCTACTG 540
 QY 582 GTTCACTCTATTTCCCAATGCACTCTCTGTGACCCCGCATGGCATGTGTGTCCTCC 641
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
 541 GTTCACTCTATTTCCCAATGCACTCTCTGTGACCCCGCATGGCATGTGTGTCCTCC 600
 QY 642 TCCCTGTG 649
 DB ||||||||
 601 TCCCTGTG 608

RESULT 6
 AAL42748
 ID AAL42748 standard; cDNA; 608 BP.
 XX AC AAL42748;
 XX AC AAL42748;
 XX 19-JUL-2002 (first entry)
 XX Human serine protease inhibitor (serpin) coding sequence 2.
 DE Human; serine protease inhibitors; serpin; blood coagulation;
 KW proteinase-activated physiological process; gene therapy;
 KW antiseptic therapy; cancer; inflammation; neurological disease;
 KW immune disease; gene; ss.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 XX CDS 1..606
 FT /*tag= a
 FT /product= "Human serpin protein 2"
 FT /transl_except= (pos: 91..93, aa: Xaa)
 FT /transl_except= (pos: 94..96, aa: Xaa)
 FT /transl_except= (pos: 97..99, aa: Xaa)
 FT /transl_except= (pos: 99..99, aa: Xaa)
 FT /note= "Xaa is unknown"

WO200155390-A1.
 XX 02-AUG-2001.
 XX 26-JAN-2001; 2001WO-US02484.

582 GTTCACTATTCCCAATGCAACTCTCTGTGACCCCGCATGGCATGTGTGTCCTCC 641
541 GTTCACTATTCCCAATGCAACTCTCTGTGACCCCGCATGGCATGTGTGTCCTCC 600
642 TCCCTGTG 649
601 TCCCTGTG 608
RESULT 7
ABK94967
ID ABK94967 standard; CDNA; 943 BP.
AC ABK94967;
XX 30-AUG-2002 (first entry)
DT Human novel polynucleotide #78.
DE
XX Human; gene; ss; inflammatory condition; shock; sepsis; immune response;
XX cancer; wound healing; central nervous system disease; haematopoiesis;
XX peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
XX myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
XX cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
XX bone degenerative disorder; periodontal disease; reperfusion injury;
XX lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
XX allergic condition; thrombolysis; thrombosis; coagulation disorder;
XX fungal infection.
OS Homo sapiens.
XX WO200244340-A2.
XX 06-JUN-2002.
XX 30-NOV-2001; 2001WO-US47004.
XX 30-NOV-2000; 2000US-0028952.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;
XX Yamazaki V, Ujwal ML, Dmanac RT;
XX WPI; 2002-508509/54.
XX P-PSDB; ABG66743.
XX Novel nucleic acids and polypeptides for diagnosis, treatment of
XX inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
XX disorders, cancer and promoting wound healing -
XX Claim 1; Page 524-525; 672pp; English.
XX The invention relates to human novel polynucleotides and associated
XX polypeptides. The polynucleotides and polypeptides are useful for
XX treating inflammatory conditions such as arthritis, nephritis, Crohn's
XX disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
XX and cancer and for promoting wound healing. The sequences are used to
XX induce the proliferation of neural cells and regeneration of nerve and
XX brain tissue, and are useful for the treatment of central and peripheral
XX nervous system diseases and neuropathies, such as Alzheimer's disease,
XX Parkinson's disease, Huntington's disease and amyotrophic lateral
XX sclerosis. The sequences are involved in chemotactic or chemokinetic
XX activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
XX cell disorders and platelet disorders such as thrombocytopenia,
XX regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
XX growth, tissue repair, healing of burns, incisions, ulcers, treatment of
XX osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
XX disease. The sequences of the invention are also useful for gut
XX protection or regeneration and treatment of lung or liver fibrosis,
XX reperfusion injury in various tissues, immune deficiencies and disorders
XX including severe combined immunodeficiency (SCID), bacterial or fungal
XX infections, autoimmune disorders e.g. multiple sclerosis and myasthenia

XX 28-JAN-2000; 2000US-0178769.
XX 29-FEB-2000; 2000WO-US05082.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ni J, Ruben SM, Shi Y;
XX WPI; 2001-457730/49.
XX P-PSDB; AA014922.
XX Isolated serine protease inhibitor polypeptide for treating, preventing
XX and/or prognosing cancers, inflammation, immune disorders and
XX neurological diseases and also for testing and detection e.g. diagnosis
XX Claim 1; Page 15; 288pp; English.
XX The invention comprises the amino acid and coding sequences of a group of
XX novel human serine protease inhibitors (serpins). Serpins are a
XX superfamily of single chain proteins that contain a conserved structure
XX of approximately 370-420 amino acids and generally range between 50 and
XX 100 kDa in molecular mass. The majority of serpins function as protease
XX inhibitors and so are involved in the regulation of several proteinase-
XX activated physiological processes (e.g. blood coagulation). The Serpin
XX DNA and amino acid sequences of the invention are useful in the treatment
XX (e.g. gene therapy, antisense therapy) and diagnosis of conditions such
XX as cancer, inflammation, neurological diseases and immune diseases. The
XX present cDNA sequence represents a human serpin coding sequence of the
XX invention.
XX Sequence 608 BP; 171 A; 141 C; 122 G; 164 T; 10 other;
Query Match 81.7%; Score 577; DB 23; Length 608;
Best Local Similarity 98.4%; Pred. No. 4.1e-161;
Matches 598; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
52 ATGGATGCTCTATCAGCAAGCAATGCGACATTTGCAATTAACCTTTTGAAGAGCTAGGG 111
1 ATGGATGCTCTATCAGCAAGCAATGCGACATTTGCAATTAACCTTTTGAAGAGCTAGGG 60
112 GAAACAACTCAACAACTTATTTTTC-----CCCATGAGCATATCATCAGCC 161
61 GAAACAACTCAACAACTTATTTTTCNNNNNNNNNNCCCATGAGCATATCATCAGCC 120
162 TTGGCCATGTTTTCATGGGGCAAGGAAACACTGCAGCTCAGATGCTCAGGCACCT 221
121 TTGGCCATGTTTTCATGGGGCAAGGAAACACTGCAGCTCAGATGCTCAGGCACCT 180
222 TGTTTTAGTAAATCGGAGGTGAAGATGGAGATATTTCATCGAGGTTTTCAGTCACCTTCT 281
181 TGTTTATGTAATCGGAGGTGAAGATGGAGATATTTCATCGAGGTTTTCAGTCACCTTCT 240
282 GTTGCAATTAAACAGACTGACATGATATGCTGTAGAACTGCCAACGGGCTCTTGA 341
241 GTTGCAATTAAACAGACTGACATGATATGCTGTAGAACTGCCAACGGGCTCTTGA 300
342 GAAAGTCTTATGATTTCCCTCAGAGTTTACAGATTCCTGTGCAAAATTTTACCAAGCA 401
301 GAAAGTCTTATGATTTCCCTCAGAGTTTACAGATTCCTGTGCAAAATTTTACCAAGCA 360
402 ACGATAAAACAGCTAGACTTTTGTGAATGATACAGAGAGTCCCAACACGTGTAAACTCC 461
361 ACGATAAAACAGCTAGACTTTTGTGAATGATACAGAGAGTCCCAACACGTGTAAACTCC 420
462 TGGTTCTGATTAACAACTGAACTGAAATTTTCAACAGAGCTGTACATCTGGAG 521
421 TGGTTCTGATTAACAACTGAACTGAAATTTTCAACAGAGCTGTACATCTGGAG 480
522 GAGCCAGGATCGGCTCTTCTCTTGTACTGCAAGCCTGCGCTTTTACAGCCCTTACTG 581
481 GAGCCAGGATCGGCTCTTCTCTTGTACTGCAAGCCTGCGCTTTTACAGCCCTTACTG 540

CC gravis, allergic conditions such as asthma, thrombolysis or thrombosis
 CC and coagulation disorders. Sequences ABK94890-ABK94982 represent human
 CC novel polynucleotides of the invention.

XX SQ Sequence 943 BP; 271 A; 214 C; 186 G; 272 T; 0 other;

Query Match 65.6%; Score 462.8; DB 24; Length 943;
 Best Local Similarity 98.4%; Pred. No. 4.2e-127;
 Matches 478; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 9 CTTTCGCTCTGGGAGCTGGCGAGAACTGGGGCTCACCGTCATGGATCTATCAGA 68
 DB 146 CTTTCGCTCTGGGAGCTGGCGAGAACTGGGGCTCACCGTCATGGATCTATCAGA 205

QY 69 AGCAATGGCACATTTGCAATTAACCTTTTGAAGAGCTAGGGGAAACAACTCAACAA 128
 DB 206 AGCAATGGCACATTTGCAATTAACCTTTTGAAGAGCTAGGGGAAACAACTCAACAA 265

QY 129 CTTATTTTTCCTCCCA-TGAGCATATCATCAGCCTTGGCCATGGTTTTCATGGGGCAAA 187
 DB 266 CTTATTTTTCCTCCCACTGAGCATATCATCAGCCTTGGCCATGGTTTTCATGGGGCAAA 325

QY 188 GGGAAACACTGCAGCTCAGATGCTCAGGCACCTTTCTTTAGTAAATCGAGGTGAAGA 247
 DB 326 GGGAAACACTGCAGCTCAGATGCTCAGGCACCTTTCTTTAGTAAATCGAGGTGAAGA 385

QY 248 TGAGATATTCATCGAGGTTTTCAGTCACCTTTCTTTGCAATTAACAGAACTGACACTGA 307
 DB 386 TGAGATATTCATCGAGGTTTTCAGTCACCTTTCTTTGCAATTAACAGAACTGACACTGA 445

QY 308 ATATGCTTAGAAGTGCACAGCGGCTCTTTGAGAAAGTCTTATGATTTCTCACAGG 367
 DB 446 ATATGCTTAGAAGTGCACAGCGGCTCTTTGAGAAAGTCTTATGATTTCTCACAGG 505

QY 368 TTTTACAGATTCCTGCGGCAATTTTACCAGCAAGTAAACACACTAGCTTTGTGAA 427
 DB 506 TTTTACAGATTCCTGCGGCAATTTTACCAGCAAGTAAACACACTAGCTTTGTGAA 565

QY 428 TGATACAGAGAGTCCACACACAGCTGTAAACTCCTGGGTTGCTGATAAAACTAAAGCCTG 487
 DB 566 TGATACAGAGAGTCCACACACAGCTGTAAACTCCTGGGTTGCTGATAAAACTAAAGTGA 625

QY 488 GAAAT 493

DB 626 AATAT 631

RESULT 8

AAF16065

ID AAF16065 standard; cDNA; 1624 BP.

AC AAF16065;

XX 13-MAR-2001 (first entry)

DT Human prostate cancer antigen nucleotide sequence SEQ ID NO: 500.

DE Human prostate cancer antigen nucleotide sequence SEQ ID NO: 500.

XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular;
 KW vulvular; gastrointestinal; nephrotropic; anti-infective; gynaecological;
 KW antibacterial; gene therapy; immune; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease; ss.

XX Homo sapiens.

OS WO200055174-A1.

PN 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05988.

XX 12-MAR-1999; 99US-0124270.

PF

XX

PR

XX (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.

XX Rosen CA, Ruben SM;

XX WPI; 2000-587513/55.

DR P-PSDB; AAB56862.

XX

PT Prostate cancer associated gene sequences, referred to as prostate
 PT cancer antigens, useful for treatment, prevention, and diagnosis of
 PT disorders such as prostate cancer -

XX Claim 1; Page 967; 2338pp; English.

XX

CC AAF15566 to AAF16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytosolic,
 CC cardioactive, immunomodulatory, muscular, vulvular, gastrointestinal,
 CC nephrotropic, anti-infective, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 1624 BP; 414 A; 421 C; 430 G; 356 T; 3 other;

Query Match 35.6%; Score 251.2; DB 21; Length 1624;

Best Local Similarity 73.6%; Pred. No. 3.9e-64;

Matches 346; Conservative 1; Mismatches 119; Indels 4; Gaps 2;

QY 15 TCCTGGGAGAGTGGCGGAGAACTGGGCTCACCGCTCATGGATGCTCTATCAGAGCAAA 74

DB 277 TTCTGCTCGCTCCCGCTCTGGAGTCTGCCATCATGGATGTTCTCGCAGAGCAAA 336

QY 75 TGGCAGATTTGCAATTAACCTTTTGAAGAGTGGGAAACAACTCAAACTATTAT 134

DB 337 TGGCAGCTTTGCTTTAAACCTTTTGAAGAGTGGGTAAGAGCAACTCGAAGATGTGT 396

QY 135 TTTTTC-CCCATGAGCATATCATCAGCTTGGCCATGGTTTTCATGGGGGCAAGGAAA 193

DB 397 TTTCTACCCATGAGCATGTCTGTGCTTGGCCATGGTCTACATGGGGGCAAGGAAA 456

QY 194 CACTGCAGCTCAGATGCTCAGGCACTTTGTTTTAGTAAATCGGAGGTGAAGATGGAGA 253

DB 457 CACGCTGCACAGATGGCCAGATACCTTTCTTCAATAAAGTGGCGGT--GGTGGAGA 513

QY 254 TATTCATCGAGGTTTTCAGTCACTTCTTGTGCAATTAACAGAACTGACACTGAATATGT 313

DB 514 CATCCACAGGCGCTTCCAGTCTCTTCTCACCAAGTGAACAGACTGCGCAGCTACTT 573

QY 314 GCTTAGAAGTCCCAACGGGCTCTTTGGAGAAAAGTCTTATGATTTTCTCACAGGTTTAC 373

DB 574 GCTTAGGATGGCCAAACAGGCTCTTTGGGAAAAGTCTTGTGATTTCTCTCATCTTTAG 633

QY 374 AGATTCTCTGTGGCAAAATTTCTACCAAGCAACGATAAACAGCTAGACTTTGTGAATGATAC 433

DB 634 AGATTCTCTGCAAAAAATTTCTACCAAGCAGAGATGGAGGCTTGAATTTATCAGGCGCGT 693

QY 434 AGAGAAAGTCCCAACAGCTGTAAACTCTCTGGGTTGCTGATAAATAAAG 483

DB 694 AGAGAAAGTCCCAACAGCTGTAAACTCTCTGGGTTGCTGATAAATAAAG 743

RESULT 9

AAS06075

ID AAS06075 standard; DNA; 695 BP.

XX

AC AAS06075;
 XX 12-SEP-2001 (first entry)
 XX Angiotensin converting enzyme (ACEV) splice variant DNA #75.
 DE XX
 KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
 KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
 KW platelet-derived endothelial cell growth factor; cardiovascular disease;
 KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; ds;
 KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
 KW myocardial infarction; coronary arterial thrombosis; renal disease;
 KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
 KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
 KW nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
 KW vascular disorder; asbestosis.
 XX
 OS Homo sapiens.
 XX
 XX WO200136632-A2.
 XX 25-MAY-2001.
 XX 17-NOV-2000; 2000WO-IL00766.
 XX 17-NOV-1999; 99IL-0132978.
 XX 10-DEC-1999; 99IL-0133455.
 XX (COMP-) COMPUGEN LTD.
 XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
 XX WPI: 2001-336004/35.
 XX P-PSDB; AAU02975.
 XX Novel alternative splicing variants e.g. variant of angiotensin
 XX converting enzyme (ACEV), useful in identifying candidate compounds
 XX capable of binding to the variant and to detect anti-variant antibodies
 XX
 XX Claim 1; Page 367; 519pp; English.
 XX The sequence represents a DNA encoding an angiotensin converting enzyme
 XX splice variant (ACEV) polypeptide. The polypeptides of the invention
 XX include variants of granulocyte colony stimulating factor receptor,
 XX glucagon, interleukin 6, platelet-derived endothelial cell growth factor,
 XX cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and
 XX vasoactive intestinal polypeptide receptor 2. The polypeptides and their
 XX associated nucleic acids are useful for identification of variant
 XX sequences and detection of candidate compounds capable of binding the
 XX molecules. The sequences of the invention can be used in the treatment
 XX and diagnosis of various disorders including cardiovascular diseases such
 XX as arteriosclerosis, myocardial infarction and coronary arterial
 XX thrombosis, renal diseases such as diabetic nephropathy, muscular
 XX diseases such as hypertrophy, immune disorders such as immune complex
 XX nephritis, multiple sclerosis, cancer, sarcoidosis, nonaroidotic
 XX pulmonary granulomatous diseases such as asbestosis and vascular
 XX pathologies involving an endothelial abnormality such as deep vein
 XX thrombosis.
 XX
 XX Sequence 695 BP; 184 A; 158 C; 154 G; 199 T; 0 other;
 XX
 XX Query Match 35.5%; Score 250.4; DB 22; Length 695;
 XX Best Local Similarity 75.4%; Pred. No. 4.5e-64;
 XX Matches 338; Conservative 0; Mismatches 106; Indels 4; Gaps 2;
 XX
 QY 37 CTGGGGCTCAGCTCATGATGCTCTATCAGAGCAATGGACATTCGATTAACCTT 96
 XX
 Db 60 CTGGGCTCTGCCATCATGATGCTCTCTCGCAGAGCAATGGACCTTGCCTTAAACCTT 119
 XX
 QY 97 TTGAAAGCTAGGGGAAACAACTCAAACTATTTTTC-CCCATGAGCATATCA 155
 XX
 Db 120 TTGAAAGCTAGGGGAAACAACTCAAACTATTTTTC-CCCATGAGCATATCC 179
 XX

156 TCAGCCTTGGCCATGGTTTTTCATGGGGCAAAAGGAAACACTGCAGCTCAGATGTCTCAG 215
 Db 180 TGTGCCCTGGCCATGGTCTACATGGGGCAAAAGGAAACACCGCTGCACAGATGCCCCAG 239
 QY 216 GCATTTTCTTTAGTAAATCGAGGTGAAGATGGAGATATTCATCGAGGTTTTCAGTCA 275
 Db 240 ATACTTTCTTTCAATAAAAGTGGCGGT---GGTGGAGACATCCACAGGGGTTCCAGTCT 296
 QY 276 CTTCTTGTGCAATTAACAGAACTGACACTGAATATGCTTAGAACTGCCAACGGGCTC 335
 Db 297 CTTCTCACCCGAAGTGAAACAGACTGGCAGCAGTACTTCTCTAGATGGCCCAACAGGCTC 356
 QY 336 TTTGAGAGAAAGTCTTATGATTTCTCTACAGGTTTACAGATTTCTGTGGCAAAATTTCTAC 395
 Db 357 TTTGGGAAAAGTCTTGTGATTTCTCTCATCTTTTAGAGATTTCTGCCAAAATTTCTAC 416
 QY 396 CAAGCAACGATAAAACAGCTAGACTTTGTGAATAGATACAGAGAACTCCACACAGTGTA 455
 Db 417 CAAGCAGAGATGGAGGAGCTTTGACTTTATCAGCGCGGTAGAGAGTCCAGAAACACATA 476
 QY 456 AACTCTCTGGTGTGATATAAACTAAAG 483
 Db 477 AACACCTGGTAGCTGAAAGACAGAGAAG 504

RESULT 10
 AAS06074
 ID AAS06074 standard; DNA; 868 BP.
 XX
 XX AAS06074;
 XX AC
 XX 12-SEP-2001 (first entry)
 XX
 XX Angiotensin converting enzyme (ACEV) splice variant DNA #74.
 XX
 KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
 KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
 KW platelet-derived endothelial cell growth factor; cardiovascular disease;
 KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; ds;
 KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
 KW myocardial infarction; coronary arterial thrombosis; renal disease;
 KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
 KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
 KW nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
 KW vascular disorder; asbestosis.
 XX
 OS Homo sapiens.
 XX
 XX WO200136632-A2.
 XX 25-MAY-2001.
 XX 17-NOV-2000; 2000WO-IL00766.
 XX 17-NOV-1999; 99IL-0132978.
 XX 10-DEC-1999; 99IL-0133455.
 XX (COMP-) COMPUGEN LTD.
 XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
 XX WPI: 2001-336004/35.
 XX P-PSDB; AAU02974.
 XX Novel alternative splicing variants e.g. variant of angiotensin
 XX converting enzyme (ACEV), useful in identifying candidate compounds
 XX capable of binding to the variant and to detect anti-variant antibodies
 XX
 XX Claim 1; Page 366; 519pp; English.
 XX The sequence represents a DNA encoding an angiotensin converting enzyme

splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P33, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarclototic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis.

Sequence 868 BP; 214 A; 212 C; 227 G; 215 T; 0 other;

Dry Match 35.5%; Score 250.4; DB 22; Length 868;
 Best Local Similarity 75.4%; Pred. No. 5e-64;
 Matches 338; Conservative 0; Mismatches 106; Indels 4;

Qy	37	CTGGGGCTCA	CGCTCATGGATGCTCTATCAGAAGCAAAATGGCACATTTTGCAATTAACCTT	96
Db	60	CTTGGGTC	TGGCCATCATGGATGTTCTCGCAGAAGCAAAATGGCACCTTTGCCTTAAACCTT	119
Qy	97	TTGAAAAGCT	TAGGGGAAAACAACCTCAAAACAACTATTATTTTTC-CCCATGAGCATATCA	155
Db	120	TTGAAAACGCT	TGGGTAAAGACAACTCGAAGAATGTGTTTTCTCACCCATGAGCATGCC	179
Qy	156	TCAGCCTTGGCCAT	TGGTTTTTCATGGGGCAAAAGGGAACACTGCAAGCTCAGATGTCTCAG	215
Db	180	TGTGCCCTGGCCAT	TGGTCTACATGGGGCAAAAGGGAACACCGCTGCACAGATGCCCCAG	239
Qy	216	GCATTTGTTTTT	TAGTAAATCGGAGGTGAAGATGGAGATATTCATCGAGGTTTTTCAGTCA	275
Db	240	ATACTTTCTTTT	CAATAAAGTGGCGGT---GGTGGAGACATCCACAGGGGCTTCAGGTCT	296
Qy	276	CTTCTTGTCAA	TAAACAGAACTGCACACTCAATATGTGCTTAGAACTGCCAACGGGGTC	335
Db	297	CTTCTCACCGA	AGTGAACAAGACTGGCAGCGCAGTACTTGCTTAGGATGCCCAACAGGGTC	356
Qy	336	TTTGGAGAAAAGT	CTTATGATTTCTCTACAGGTTTTACAGATTTCTGTGGCAAAATTCAC	395
Db	357	TTTGGGAAAAGT	CTTGGAATTTCTCTCATCTTTTAGAGATTTCTGCGCAAAAATTCAC	416
Qy	396	CAAGCAACGAT	AAAAACAGCTAGACTTTGTGTAATGATACAGAGAGAGTCCACACACGTCGA	455
Db	417	CAAGCAGAGAT	TGGAGGAGCTTGACTTTATCAGCGCGGTAGAGAAAGTCCAGAAAACACATA	476
Qy	456	AACCTCTGGGT	TGCTGATAAAACTAAAG	483
Db	477	AACACCTGGGT	AGCTGAAAAGACAGAAG	504

RESULT 11

AAS06073
ID AAS06073 standard; DNA: 1302 BP.

AC AAS06073;

DT 12-SEP-2001 (first entry)

DE Angiotensin converting enzyme (ACEV) splice variant DNA #73.

Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
platelet-derived endothelial cell growth factor; glucovascular diseases;
cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C; ds;
vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
myocardial infarction; coronary arterial thrombosis; renal disease;
diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;

multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcolotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.

Homo sapiens.

WO200136632-A2.

25-MAY-2001.

17-NOV-2000:

17-NOV-1999: . 99IL-0132978.

10-DEC-1999; 99IL-0133455.

(COMP -) COMPUGEN LTD.

Levine Z, David A, Azar I, Khosravi R, Bernstein J;

WPI; 2001-336004/35.

100

converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies

Claim 1; Page 366; 519pp; English.

The sequence represents a DNA encoding an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen p53, and vasointestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonaroidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis.

Sequence 1302 BP; 341 A; 305 C; 345 G; 311 T; 0 other;

```
Query Match      35.5%; Score 250.4; DB 22; Length 1302;
Best Local Similarity 75.4%; Pred. No. 6.1e-64;
Matches 338; Conservative 0; Mismatches 106; Indels 4; Gaps 2;
```

QY 37 CTGGGGCTCACCGTCATGGATGCTCTATCAGAAGCAAATGGCACATTTGCGATTAAACCTT 96

Db
60 CTTGGGTCTGCCATCATGGATGTTCTCGCAGAACCAATGGCACCTTTGCCTTAAACCTT 11

97 TTGAAAAAGCTAGGGGAAAACAACTCAAAACAATTATTTTTC-CCCATGAGCATATCA 155

120 TTGAAAACGCTGGGTAAAGACAACTCGAAGAAATGTGTTTTCTCACCCATGAGCATGTCC 179

156 TCAGCCTTGGCCATGGTTTCAATGGGGCCAAAGCCGAAACATGTCACGCTACATCTCTCTACG 315

180 TGTGGCCCTGGCCATGGTCTACATGGGCGAAGCGAACAACCCCTCCACACATCCCGC

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QY 336 TTTGGAGAAAAGCTTTATGATTCTTCTCACAGGTTTTTACAGATTCCTGTGGCAAAATTTCTAC 395
 DB 357 TTTGGGAAAAGCTTTGATTTCTCTCACTTTTATAGATTCCTGCCAAAATTTCTAC 416
 QY 396 CAAGCAACGATAAAAACAGCTAGACTTTTGTGAATGATACAGAGAAAGTCCACAAACAGTGTA 455
 DB 417 CAAGCAGAGATGAGGAGCTTGACITTTATCAGCGCGGTAGAGAGTCCAGAAAACACATA 476
 QY 456 AACTCTCGGTGCTGATAAAACTAAAG 483
 DB 477 AACACTCGGTAGCTGAAAAGACAGAAG 504

RESULT 12

ID AAF23495 standard; DNA; 1366 BP.

AC AAF23495;

DT 22-MAR-2001 (first entry)

XX Thrombin inhibitor DNA.

XX Thrombin inhibitor; neurodegenerative disease; Alzheimer's;

XX Parkinson's; tumour; deep venous thrombosis; pulmonary embolism;

XX heart; ss.

XX Unidentified.

OS US6156540-A.

XX 05-DEC-2000.

XX 22-DEC-1993; 93US-0171817.

XX 22-DEC-1993; 93US-0171817.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Fuldner RA, Cao L, Adams MD;

XX WPI; 2001-060165/07.

XX Novel polynucleotide encoding thrombin inhibitor polypeptide useful for

XX diagnosis and treatment of diseases related to thrombosis -

XX Claim 13; Fig.1; 19pp; English.

XX The present invention relates to a thrombin inhibitor. This is useful

XX for diagnosis and treatment of thrombosis, neurodegenerative diseases

XX such as Alzheimer's disease and Parkinson's disease, tumor metastasis,

XX to prevent proximal extension of deep venous thrombosis or the

XX recurrence of pulmonary embolisms and also to treat risk patients who

XX have congestive heart failure, acute myocardial infarction or

XX cardiomyopathy to prevent the development of deep vein thrombosis or

XX pulmonary embolism. The thrombin inhibitor is also useful for

XX screening chemical compounds that either up or down regulate its

XX activity.

XX Sequence 1366 BP; 360 A; 332 C; 355 G; 317 T; 2 other;

SQ Query Match 35.3%; Score 249.2; DB 22; Length 1366;

Best Local Similarity 73.4%; Pred. No. 1.4e-63;

Matches 345; Conservative 1; Mismatches 120; Indels 4; Gaps 2;

QY 15 TCGTGGCAGCTCGCGGAGAACTGGGGCTCCCGTCATGGATGCTTATCAGAGCAAA 74

DB 40 TTTCTGCTCGCTCGCTCCCGCTCTGGAGTCTGCCATCATGGATGTTCTGCAGAGCAAA 99

QY 75 TGGCATTGTCATTAAACCTTTTGAAGAGCTAGGGGAAAACAACTCAAACTTATT 134

DB 100 TGGCACCTTTGCTTAAACCTTTTGAAGAGCTAGGGGAAAACAACTCGAAGATGTGT 159

QY 135 TTTTTC-CCCATGAGCATATCATCAGCCTTTGGCCATGTTTTCATGGGGCAAAAGGAAA 193
 DB 160 TTTCTCACCCATGAGCATGCTGTGCTTGGCCATGTTTACATGGGGCAAAAGGAAA 219
 QY 194 CACTGCAGCTCAGATGCTCAGGCACCTTTTGTAGTAAATCGAGGTGAGATGAGA 253
 DB 220 CACGCTGCACAGATGCCCGCAGATACCTTTCTTCAATAAAGTGCGCGTG--GTGGAGA 276
 QY 254 TATTTCATCGAGGTTTTCAGTCACCTTCTTGTGCAATTAACAGAACTGACACTGAATATGT 313
 DB 277 CATCCACAGGGCTTCCAGTCTTCTTACCGAAGTGAACAGACTGGCCAGCAGTACTT 336
 QY 314 GCTTAGAACTGCCAACGGGCTCTTTGGAGAAAAGCTTTATGATTTCTTCACAGGTTTAC 373
 DB 337 GCTTAGGATGCCCAACAGGCTCTTTGGGAAAAGCTTTGTGATTTCTCTCATCTTTAG 396
 QY 374 AGATTCCTGTGGCAAAATTTTACCAAGCAACGATAAAACAGCTAGACTTTGTGAATGATAC 433
 DB 397 AGATTCCTGTGGCAAAATTTTACCAAGCAAGATGGAGAGCTTGACTTTATCAGCGCGT 456
 QY 434 AGAGAAGTCCCAACACGCTGTAAACTCTCTGGTTGCTGTATAAACTAAAG 483
 DB 457 AGAGAAGTCCCAACACATATAAACACTGGGTAGCTGAAAAGACAGAG 506

RESULT 13

AAC65737

ID AAC65737 standard; cDNA; 1366 BP.

XX AAC65737;

AC AAC65737;

XX 16-FEB-2001 (first entry)

DT Human thrombin inhibitor cDNA.

XX Thrombin inhibitor; human; thrombolytic; cardiant; cytostatic; nootropic;

XX KW neuroprotective; antiparkinsonian; gene therapy; treatment; carcinoma;

XX KW cell hypercoagulation; deep venous thrombosis; pulmonary embolism;

XX KW cerebral embolism; thrombic disease; tumor metastases; clot accretion;

XX KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease; ss.

XX OS Homo sapiens.

XX US6133422-A.

XX 17-OCT-2000.

XX 30-NOV-1998; 98US-0200965.

XX 22-DEC-1993; 93US-0171817.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Fuldner RA, Rosen CA, Cao L, Adams MD;

XX WPI; 2001-006150/01.

XX P-PSDB; AAB11125.

XX New thrombin inhibiting proteins for treating or preventing

XX thrombosis-related diseases, e.g. embolism, tumor metastases,

XX PT carcinoma, neurodegenerative diseases, e.g. Alzheimer's or Parkinson's

XX disease -

XX Example 1; Column 15-16; 19pp; English.

XX This invention describes a novel human thrombin inhibitor which has

XX thrombolytic, cardiant, cytostatic, nootropic, neuroprotective and

XX antiparkinsonian activity and can be used for gene therapy. The thrombin

XX inhibitor may be used therapeutically or diagnostically to treat or

XX prevent diseases related to thrombosis characterized by hypercoagulation

XX of cells. The protein may also be used to prevent extension of deep

XX venous thrombosis of the recurrence of pulmonary embolisms and

XX recurrence of cerebral or other systemic embolisms, to treat high risk

Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
platelet-derived endothelial cell growth factor; cardiovascular disease;
cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; ds;
vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
myocardial infarction; coronary arterial thrombosis; renal disease;
diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
multiple sclerosis; immune complex nephritis; deep vein thrombosis;
nonrheumatoid pulmonary granulomatous disease; endothelial abnormality;

Query Match	35.0%	Score	246.8	DB	22	Length	1324
Best Local Similarity	75.8%	Pred. No.	7,2e-63				
Matches	332	Conservative	0	Mismatches	102	Indels	4
		Gaps	2				
QY	47	CCGTCATGGATGCTCTATCAGAAGCAAAATGGCACACATTTTGCATTAAACCTTTTGGAAAAAGC	106				
Db	204	CCATCATGGATGTTCTCGCAGAAGCAAAATGGCACCTTTGGCCTTAAACCTTTTGGAAACGC	263				
QY	107	TAGGGGAAAACAACCTCAAAACAATTATTTTTTTC-CCCATGAGCATATCATCAGCCCTTGG	165				
Db	264	TGGGTAAGACAACCTCGAAGAAATGTGTTTTTCTACCCATGAGCATGTCCTGTGCCCTGG	323				
QY	166	CCATGTTTTTCATGGGGCAAAAGGGAACACATGCACTCAGATGCAGATGTCAGGCACCTTTGTT	225				
Db	324	CCATGGTCTACATGGGGGCAAAAGGGAACACCGCTGCA CAGATGGCCACAGATACTTTCTT	383				
QY	226	TTAGTAAATCGGAGGTGAAGATGGAGATATTTCATCGAGGTTTTTTCAGTCACTTCTTGTTG	285				
Db	384	TCAATAAAAGTGGCGT---GGTGGAGACATCCACGGGTTCCAGTCTCTTCTCAACG	440				
QY	286	CAATTAAACAGACTGACACTGAATATGTCTTAGAACTGCCACGGGCTCTTTGGAGAAA	345				
Db	441	AAGTGAAACAAGACTGCAACCGAGTACTTGCTTTAGGGTGGCCACAGAGCTCTTTGGGGAAA	500				
QY	346	AGTCTTATGATTTCTTCACAGTTTTACAGATTCTGTGGCAAAATTCACCAAGCAACGA	405				

CC	.	thrombolysis.
XX	Sequence	1349_BP; 370_A; 298_C; 358_G; 323_T; 0_other;
SQ		
	Query Match	35.0%; Score 246.8; DB 22; Length 1349;
	Best Local Similarity	75.8%; Pred. No. 7.2e-63;
	Matches 332; Conservative	0; Mismatches 102; Indels 4; Gaps 2;
QY	47	CGCTCATGGATGCTCTATCAGAAACCAATGGCACATTTCATTAAAACCTTTTGAAAAAGC 106
DB	204	CCAATCATGGNATGTCTCGCNAGAACHAATGGCACTTTCCTTAACACTTTTGAAAAACGC 263
QY	107	TAGGGGAAAAACAATCAAACAACCTTAATTTTTTC - CCCATGACATATCATCAGCCTTGG 165
DB	264	TGGGTAAAGAACAACTCGAAGAATGTGTCTTCTCACCCATGAGCATGTCTGTGCCCTGG 323
QY	166	CCATGGTTTTTCATGGGGCAAGGAACCCTGAGCTCAGATGTCTCAGGCACATTTGTT 225
DB	324	CCATGGTCTACATGGGGCCAAAGGAAACACCCGCTGCACAGATGGCCACAGATACTTCTT 383
QY	226	TTAGTAAATCGGAGGTGAAGATGGAGATATTCATCGAGGTTTTCAGTCACTTCTTGTG 285
DB	384	TCAATAAAGTGCGCGT --GGTGGAGACATCACCCAGGGCTTCCAGTCTCTTCTCACCG 440
QY	286	CNAATTACGAACCTGCACATGAATATCTGCTTAGAACTGCCAACGGGCTCTTTGAGAGAA 345
DB	441	AAGTGAACAAGACTGGCACCGCAGTACTTGCTTAGGGTGGCCACACAGGCTCTTTGGGAAA 500
QY	346	AGTCTTATGATTCCTCACAGGTTTTACAGATTCCTGTGGCAANTTCTACCAAGCAAGA 405
DB	501	AGTCTTGTGATTCCTCTCATCTTTTAGAGATTCTCTGCCAAAAATTTACCAAGCAGAGA 560
QY	406	TAAACACGCTAGACTTTGTGAATCATACAGAGAAAGTCCACAACACGCTGTAAACTCCTGGG 465
DB	561	TGGAGGAGCTTGACTTTATCAGCCCGTAGAGAAGTCAGAGAAACACATAAACACCTGGG 620
QY	466	TTGCTGATAAAACTAAAG 483
DB	621	TAGCTGRAAAGACAGAG 638

17-NOV-1999; 99IL-0132978.
10-DEC-1999; 99IL-0133455.
(COMP-) COMPUGEN LTD.
Levine Z, David A, Azar I, Khosravi R, Bernstein J;
WPI; 2001-336004/35.
P-PSDB; AAU02922.
Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies

Claim 1; Page 327; 519pp; English.

The sequence represents a DNA encoding an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonaroidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein

Sult No.	Query No.	Score	Match	Length	DB	ID	Description
1	249.2	35.3	1366	3	US-09-200-965-1	Sequence 1, Appli	
2	214.4	30.4	1425	1	US-08-464-148-1	Sequence 1, Appli	
3	214.4	30.4	1425	1	US-08-385-500-1	Sequence 1, Appli	
4	214.4	30.4	1425	1	US-08-846-784-1	Sequence 1, Appli	
5	177.4	25.1	1393	1	US-08-464-148-3	Sequence 3, Appli	
6	177.4	25.1	1393	1	US-08-385-500-3	Sequence 3, Appli	
7	177.4	25.1	1393	1	US-08-846-784-3	Sequence 3, Appli	
8	103.2	14.6	1482	1	US-07-768-286B-5	Sequence 5, Appli	
9	84.8	12.0	1245	4	US-09-266-910-1	Sequence 1, Appli	
10	84.8	12.0	1245	4	US-09-266-910-2	Sequence 1, Appli	
11	84.8	12.0	1711	1	US-08-568-147B-1	Sequence 1, Appli	
12	77.4	11.0	1316	1	US-07-755-461A-12	Sequence 12, Appl	
13	77.4	11.0	1316	1	US-08-315-831A-12	Sequence 12, Appl	
14	77.4	11.0	1316	1	US-08-662-328-12	Sequence 12, Appl	
15	77.4	11.0	1316	5	PCR-US959-12509-12	Sequence 12, Appl	
16	76.2	10.8	1152	1	US-08-315-831A-13	Sequence 13, Appl	
17	76.2	10.8	1152	1	US-08-662-318-13	Sequence 13, Appl	
18	76.2	10.8	1152	5	PCR-US959-12509-13	Sequence 13, Appl	
19	70	9.9	1950	2	US-08-472-659-30	Sequence 30, Appl	
20	70	9.9	1950	2	US-08-474-661-30	Sequence 30, Appl	
21	70	9.9	1950	2	US-08-611-977-30	Sequence 30, Appl	
22	65.4	9.3	1308	4	US-09-123-912-109	Sequence 109, App	
23	65.4	9.3	1308	4	US-09-643-597-109	Sequence 109, App	
24	65.4	9.3	1419	4	US-09-123-912-111	Sequence 111, App	
25	65.4	9.3	1419	4	US-09-643-597-111	Sequence 111, App	
26	63.2	9.0	1512	1	US-07-768-286B-3	Sequence 3, Appli	
27	62.4	8.8	1328	1	US-07-679-052A-14	Sequence 14, Appl	

APPLICANT: Sprecher, Cindy A.
 TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
 CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESS: Townsend and Townsend Kourie and Crew
 STREET: Steuart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,148
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/385,500
 FILING DATE: 08-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Parmelee, Steven W.
 REGISTRATION NUMBER: 31,990
 REFERENCE/DOCKET NUMBER: 13952-21
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 467-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1425 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

RESULT 3
US-08-385-500-1
Sequence 1, Application US/08385500
Patent No. 5712117
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,500
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-21

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 92..1213
; OTHER INFORMATION: /product= "CYTOPLASMIC
; OTHER INFORMATION: ANTIPROTEINASE-2 PROTEIN"
US-08-385-500-1

Query Match 30.4%; Score 214.4; DB 1; Length 1425;
Best Local Similarity 73.3%; Pred. No. 3.8e-55;
Matches 321; Conservative 0; Mismatches 101; Indels 16; Gaps 3;

QY 50 TCATGGATGCTCTATCAGAAAGCAATGGCACATTTCGATTAAACCTTTGAAAAAGCTAG 109
Db |||||
QY 90 TGATGGATGACCTCTGTGAAGCAATGGCACTTTTGGCATCAGCTTATTTAAATATTGG 149
Db |||||
QY 110 GGGAAA---ACAACCTCAACAACTTATTTTTC-CCCATGAGCATATCATCAGCCTTGG 165
Db |||||
QY 150 GGGAGAGGAGCAACTCAAGAAACGTATTTCTCTCCCATGAGCATCTCTGCGCTGG 209
Db |||||
QY 166 CCATGGTTTTCATGGGGGCAAGGAAACACTGCAGCTCAGATGCTCAGGCACTTTGTT 225
Db |||||
QY 210 CCATGGTCTTCATGGGGGCAAGGAAAGCACTGCAGCCAGATGTCCCATGAGCATTTGTT 269
Db |||||
QY 226 TTAGTAAATCGAGAGTGAAGATGAGATATTCATCGAGGTTTTCAGTCACTTCTTGTG 285
Db |||||
QY 270 T-----ATCAAAAGAGCGAGATATTCACCGAGGTTTCCAGTCACTTCTCAGTG 317
Db |||||
QY 286 CAATTAACAGAACTGCACACTGAATATGTGCTTAGAACTGCCAACGGGCTCTTTGGAGAA 345
Db |||||
QY 318 AGTTAAACAGAACTGGCACTCAGTACTTGTAGAACTGCCAACAGACTCTTTGGAGAA 377
Db |||||
QY 346 AGTCTTATGATTTCTCCACAGGTTTTCAGATTCCTGTGCAAAATCTTACCAAGCAAGA 405
Db |||||
QY 378 AGAGGTGTGATTTCTCCAGACTTTAAAGAACTACTGTAGAACTTCTATCAGCAGAGC 437
Db |||||
QY 406 TAAACAGCTAGACTTTTGAATGATACAGAGAGTCCACACAGTGTAAACTCCTCGG 465
Db |||||
QY 438 TGGAGGAGTTGTCTTTTGTCTGAAGACACTGAAGAGTGCAGGAAGCATATAATGACTGG 497
Db |||||

RESULT 4
US-08-784-1
; Sequence 1, Application US/08846784
; Patent No. 5747645
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,784
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/385,500
; FILING DATE: 08-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 92..1213
; OTHER INFORMATION: /product= "CYTOPLASMIC
; OTHER INFORMATION: ANTIPROTEINASE-2 PROTEIN"
US-08-846-784-1

Query Match 30.4%; Score 214.4; DB 1; Length 1425;
Best Local Similarity 73.3%; Pred. No. 3.8e-55;
Matches 321; Conservative 0; Mismatches 101; Indels 16; Gaps 3;

QY 50 TCATGGATGCTCTATCAGAAAGCAATGGCACATTTCGATTAAACCTTTGAAAAAGCTAG 109
Db |||||
QY 90 TGATGGATGACCTCTGTGAAGCAATGGCACTTTTGGCATCAGCTTATTTAAATATTGG 149
Db |||||
QY 110 GGGAAA---ACAACCTCAACAACTTATTTTTC-CCCATGAGCATATCATCAGCCTTGG 165
Db |||||
QY 150 GGGAGAGGAGCAACTCAAGAAACGTATTTCTCTCCCATGAGCATCTCTGCGCTGG 209
Db |||||
QY 166 CCATGGTTTTCATGGGGGCAAGGAAACACTGCAGCTCAGATGCTCAGGCACTTTGTT 225
Db |||||
QY 210 CCATGGTCTTCATGGGGGCAAGGAAAGCACTGCAGCCAGATGTCCCATGAGCATTTGTT 269
Db |||||
QY 226 TTAGTAAATCGAGAGTGAAGATGAGATATTCATCGAGGTTTTCAGTCACTTCTTGTG 285
Db |||||
QY 270 T-----ATCAAAAGAGCGAGATATTCACCGAGGTTTCCAGTCACTTCTCAGTG 317
Db |||||
QY 286 CAATTAACAGAACTGCACACTGAATATGTGCTTAGAACTGCCAACGGGCTCTTTGGAGAA 345
Db |||||
QY 318 AGTTAAACAGAACTGGCACTCAGTACTTGTAGAACTGCCAACAGACTCTTTGGAGAA 377
Db |||||
QY 346 AGTCTTATGATTTCTCCACAGGTTTTCAGATTCCTGTGCAAAATCTTACCAAGCAAGA 405
Db |||||
QY 378 AGAGGTGTGATTTCTCCAGACTTTAAAGAACTACTGTAGAACTTCTATCAGCAGAGC 437
Db |||||
QY 406 TAAACAGCTAGACTTTTGAATGATACAGAGAGTCCACACAGTGTAAACTCCTCGG 465
Db |||||
QY 438 TGGAGGAGTTGTCTTTTGTCTGAAGACACTGAAGAGTGCAGGAAGCATATAATGACTGG 497
Db |||||

RESULT 5
US-08-464-148-3
; Sequence 3, Application US/08464148.
; Patent No. 5710026
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.

Db 449 ATGCTGAGCTGAAGGAGCTTTCTTTATCAGAGCTGCAGAGAGTCCAGGAAACACATCA 508
Qy 457 ACTCCTGGTGTCTGATATAAAG 483
Db 509 ACACCTGGGTCTCAAAAAGACCCGAG 535
RESULT 6
US-08-385-500-3
; Sequence 3, Application US/08385500
; Patent No. 5712117
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,500
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1393 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 112..1239
; OTHER INFORMATION: /product= "CYTOPLASMIC
; OTHER INFORMATION: ANTIPROTEINASE-3 PROTEIN"
US-08-385-500-3
Query Match 25.1%; Score 177.4; DB 1; Length 1393;
Best Local Similarity 66.0%; Pred. No. 5.8e-44;
Matches 295; Conservative 0; Mismatches 136; Indels 16; Gaps 2;
Qy 41 GGCTCACCGTCATGGATGCTCTATCAGAGCAAAATGGCAATTTGCAATTAACCTTTTGA 100
Db 101 GGCCTGTCATGGAAGTCTTTCTAATGCAAGTGTACTTTTGGCATAACGCTTTTAA 160
Qy 101 AAAAGCTAGGGGAAACAACTCAACAC-----TTATTTTTCCTCCATGAGCATATCAT 156
Db 161 AGATACTGTGTCAAGATAACCTTCGCACAACGTTCTCTCTCTGTGAGCATCTCT 220
Qy 157 CAGCCTTGGCCATGGTTTTCATGGGGCAAGGAAACACCTGCAGCTCAGATGTCACG 216
Db 221 CTGCGCTGGCCATGGTTCTCTAGGGCAAGGAAACACCGCAACCCAGATGGCCAGG 280
Qy 217 CACTTTGTTTGTAGTAAATTCGGAGGTGAAGATGGAGATATTCATCGAGTTTTCAGTCAC 276
Db 281 CACTGTCTTTAAACA-----CAGAGGAAGACATTCATCGGCTTTTCCAGTCGC 328

;; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
;; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES.
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourie and Crew
;; STREET: Steuart Street Tower, One Market Plaza
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: US
;; ZIP: 94105-1493
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/464,148
;; FILING DATE: 05-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/385,500
;; FILING DATE: 08-FEB-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; REFERENCE/DOCKET NUMBER: 13952-21
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 467-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1393 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 112..1239
;; OTHER INFORMATION: /product= "CYTOPLASMIC
;; OTHER INFORMATION: ANTIPROTEINASE-3 PROTEIN"
US-08-464-148-3
Query Match 25.1%; Score 177.4; DB 1; Length 1393;
Best Local Similarity 66.0%; Pred. No. 5.8e-44;
Matches 295; Conservative 0; Mismatches 136; Indels 16; Gaps 2;
Qy 41 GGCTCACCGTCATGGATGCTCTATCAGAGCAAAATGGCAATTTGCAATTAACCTTTTGA 100
Db 101 GGCCTGTCATGGAAGTCTTTCTAATGCAAGTGTACTTTTGGCATAACGCTTTTAA 160
Qy 101 AAAAGCTAGGGGAAACAACTCAACAC-----TTATTTTTCCTCCATGAGCATATCAT 156
Db 161 AGATACTGTGTCAAGATAACCTTCGCACAACGTTCTCTCTCTGTGAGCATCTCT 220
Qy 157 CAGCCTTGGCCATGGTTTTCATGGGGCAAGGAAACACCTGCAGCTCAGATGTCACG 216
Db 221 CTGCGCTGGCCATGGTTCTCTAGGGCAAGGAAACACCGCAACCCAGATGGCCAGG 280
Qy 217 CACTTTGTTTGTAGTAAATTCGGAGGTGAAGATGGAGATATTCATCGAGTTTTCAGTCAC 276
Db 281 CACTGTCTTTAAACA-----CAGAGGAAGACATTCATCGGCTTTTCCAGTCGC 328
Qy 277 TTCTTGTGCAATTAACAGAACTGCACACTGAATATGTCTTAGAATGCCAAGCGGCTCT 336
Db 329 TTCTCACTGAAGTGAACAGGCTGGCACAAGTCTCTGAGAACCGCCACAGGCTCT 388
Qy 337 TTGAGAGAAAGCTTTATCATTTCTCAAGGTTTACAGATTCCTGTGGCAATTTTACC 396
Db 389 TTGAGAGAAAGCTTTGTCAGTTCTCTCAAGTTTAAAGGAATCTGTCTTCAATTTACC 448
Qy 397 AAGCAACGATTAACAGCTAGACTTTTGTGAATGATACAGAGAAAGTCCACACACGTTGTA 456

QY 277 TTCTTTGTCATTAACAGAACTGACACTGAATATGTCTTTAGAACTGCCAACGGGCTCT 336
Db 329 TTCTCAGTGAAGTGAACAAAGGCTGGCACACAGTACCTGCTGAGAACGGCCAAACAGGCTCT 388
QY 337 TTGAGAAAGTCTTTATGATTTCTTCACAGGTTTACAGATTCTCTGTGGCAAAATTTCTACC 396
Db 389 TTGAGAGAAACTTGTCTCTCTCAAGTTTAAAGAAATCTCTGCTTTCAATTTCTACC 448
QY 397 AAGCAACGATAAACAGCTAGACTTTGTGAATGATACAGAGAACTCCACAAACAGCTGTAA 456
Db 449 ATGCTGAGCTGAAGGAGCTTTCTTTATCAGAGCTGCAGAGAGTCCAGGAACACATCA 508
QY 457 ACTCCTGGTGTCTGATAAACTAAAG 483
Db 509 ACACCTGGTCTCAAAAAGACCGAAG 535

RESULT 7
US-07-768-286B-5
Sequence 3, Application US/0846784
Patent No. 5747645
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,784
FILING DATE: 30-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/385,500
FILING DATE: 08-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-21
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 112..1239
OTHER INFORMATION: /product= "CYTOPLASMIC
OTHER INFORMATION: ANTIPROTEINASE-3 PROTEIN"
US-08-846-784-3

Query Match 25.1%; Score 177.4; DB 1; Length 1393;
Best Local Similarity 66.0%; Pred. No. 5.8e-44;
Matches 295; Conservative 0; Mismatches 136; Indels 16; Gaps 2;
QY 41 GGCTCACCGTCATGATGCTCTATCAGAGCAAAATGGCACATTTTCATTAACCTTTTGA 100
Db 101 GGCCCTGCATCATGGAACACTCTTCTAATGCAAGTGTACTTTTGGCATACGCCCTTTAA 160

QY 101 AAAGCTAGGGGAAACAACTCAAAACAC-----TTATTTTTTCCCCATGACATATCAT 156
Db 161 AGATACGTGTCAAGATAACCCCTTCGCACAACGTGTCTGTCTCTGTGAGCATCTCCT 220
QY 157 CAGCCCTTGCCCATGGTTTTCATGGGGGCAAGGAAACACTCAGCTCAGATGTCTCAGG 216
Db 221 CTGCCCTGGCCATGGTTCTCTTAGGGGCAAGGAAACACCCCAACCCAGATGGCCAGG 280
QY 217 CACTTTGTTTAAATTCGAGGTGAAGATGAGATATTCATCGAGGTTTTTCAGTCAC 276
Db 281 CACTGTCTTTAAACA-----CAGAGGAAGACATTTCATCGGCTTTCCAGTCGC 328
QY 277 TTCTTTGTCGAATTAACAGAACTGACACTGAATATGTCTTTAGAACTGCCAACGGGCTCT 336
Db 329 TTCTCAGTGAAGTGAACAAAGGCTGGCACACAGTACCTGCTGAGAACGGCCAAACAGGCTCT 388
QY 337 TTGAGAAAGTCTTTATGATTTCTTCACAGGTTTTCACAGATTCTCTGCGCAAAATTTCTACC 396
Db 389 TTGAGAGAAACTTGTCTCAGTTCTCTCAACGTTTAAAGAAATCTCTGCTTTCAATTTCTACC 448
QY 397 AAGCAACGATAAACAGCTAGACTTTGTGAATGATACAGAGAACTCCACAAACAGCTGTAA 456
Db 449 ATGCTGAGCTGAAGGAGCTTTCTTTATCAGAGCTGCAGAGAGTCCAGGAACACATCA 508
QY 457 ACTCCTGGTGTCTGATAAACTAAAG 483
Db 509 ACACCTGGTCTCAAAAAGACCGAAG 535

RESULT 8
US-07-768-286B-5
Sequence 5, Application US/07768286B
Patent No. 5444153
GENERAL INFORMATION:
APPLICANT: GOSS, Neil H.
APPLICANT: RICHARDSON, Michael A.
TITLE OF INVENTION: VARIANTS OF PAI-2
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/768,286B
FILING DATE: 19911011
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU90/00603
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/157 CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1482 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Homo sapiens
CELL TYPE: Monocyte
CELL LINE: U937
IMMEDIATE SOURCE: BTA 1922
CLONE: BTA 1922
FEATURE:
NAME/KEY: CDS
LOCATION: 22, 1170
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "Product binds to urokinase, tissue plasminogen activator"
OTHER INFORMATION: /product= "PAI-2 variant, protease sensitive site removed"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /notes= "Codes for human plasminogen activator inhibitor type 2 protein in which amino acids 66 to 98 inclusive have been deleted."
OTHER INFORMATION: to 98 inclusive have been deleted."
US-07-768-286B-5

Query Match 14.6%; Score 103.2; DB 1; Length 1482;
Best Local Similarity 53.9%; Pred. No. 1.6e-21;
Matches 236; Conservative 0; Mismatches 198; Indels 4; Gaps 1;

QY 52 ATGGATGCTCTATCAGAGCAATGGCACAATTTGCAATTAACCTTTTGAAGAGCTAGG 111
DB 22 ATGGAGATCTTTGTGTGGCAACACACTCTTTGGCCCTCAATTTATTCAAGCATCTGGCA 81

QY 112 GAAACCACTCAAC---AAGTTATTTTCCCATGAGATATCATCAGCTTGGCC 167
DB 82 AAGCAAGCCCAACCAAGCACTCTCTCTCCCATGAGATCTCTGTCACCATGGCC 141

QY 168 ATGGTTTTCATGGGGCAAGGAAACACTGAGCTCAGATGCTCAGGACCTTTGTTT 227
DB 142 ATGGTCTACATGGCTCCAGGGGAGCAAGCAAGCAAGCAAGCTTCAAGTTT 201

QY 228 AGTAAATCGAGTGAAGTGAATGAGATATTCATCGAGTTTTCAGTCTTCTGTGCA 287
DB 202 AATGAAGTGGAGCGCTGAGATAAATCCATTCCTTCGCTCTCTGAGTCTGCA 261

QY 288 ATTAACAGAACTGACACTGAATATGTCTTAGAATCTGCAAGCTGCAAGGCTCTTTGAGAAAAG 347
DB 262 ATCAATGCTCCACAGGGAATTTACTGGAAGTGTCAATAAGCTGTTGTGAGAAG 321

QY 348 TCTTATGATTTCTTCAAGCTTTTACAGATCTCTGAGGCAATTTCTACCAAGCAAGATA 407
DB 322 TCTGCGAGCTTCCGGGGAAGATATATTCGACTCTGTGAGAAATATTACTCTCAGAACCC 381

QY 408 AAACAGCTAGACTTTGTGAATGATACAGAGAAGTCCACACACGCTGTAAACTCTGGTT 467
DB 382 CAGCAGTGAATCTCTAGATGTGCAAGAGCTAGAAAAGATTAATCTCTGGTC 441

QY 468 GCTGATAAACTAAAGCC 485
DB 442 AAGACTCAACCAAGGC 459

RESULT 9
US-09-266-910-1
Sequence 1, Application US/09266910
Patent No. 6344362
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Use of a recombinant protein as receptor of a hepatitis virus
NUMBER OF SEQUENCES: 8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,910
FILING DATE:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,910
FILING DATE:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1245 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Squamous Cell Carcinoma Antigen
TISSUE TYPE: Hepatoma
CELL TYPE: Hepatocyte
CELL LINE: HepG2
US-09-266-910-1

Query Match 12.0%; Score 84.8; DB 4; Length 1245;
Best Local Similarity 53.4%; Pred. No. 5.3e-16;
Matches 251; Conservative 0; Mismatches 182; Indels 37; Gaps 2;

QY 51 CATGGATGCTCTATCAGAGCAATGGCACAATTTGCAATTAACCTTTTGAAGAGCTAGG 110
DB 7 CATGAATTCATCTAGTGAAGCCACACCAAGTTTCATGTTCCAGCTGTTCACACAGTTTCAAG 66

QY 111 GGAACCACTCAACCAACTTATTTTTCCTCC-ATGAGCATATCATCAGCTTGGCCAT 169
DB 67 AAAATCAAGAGAACCAACATCTTCTATTTCCCTATCAGCATCACATCAGCATTTAGGAT 126

QY 170 GGTTCATGGGGCAAGGAAACACTGAGCTCAGATGCTCAGGACCTTTGTTTGTAG 229
DB 127 GGTCTCTTAGAGCCAAAGACAACTGACACAGATTAAAGAGGTTCTTCACTTTGA 186

QY 230 TAAATCGAGGTGAAGT-----GGAGA 253
DB 187 TCAAGTCACAGAGAACACACAGGAAAGTGAACATATCATGTTGATAGTCAGGAAA 246

QY 254 TATTTCATCGAGTTTTCAGTCACTTCTTTGTCGAATTAACAGAACTGACACTGAATATGT 313
DB 247 TGTTCATCACCAGTTTCAAAAGCTTCTGACTGAATTAACAAATCCACTGATGATATGA 306

QY 314 GCTTAGAAGTCCCAACAGGCTCTTTGGAGAAAAGTCTTATGATTTCTCAGGTTTAC 373
DB 307 GCTGAAGATCCCAACAGCTCTTCGGAGAAAAAAGCGTATCTATTTTACAGGAATATT 366

QY 374 AGATTCTCTGCGAAATTTCTACCAAGCAACGATAAACAGCTAGACTTTGTGAATGATAC 433
DB 367 AGATGCCATCAAGAAATTTTACCAAGCCAGTGTGGAATCTGTTGTTTGCATTTGCTCC 426

QY 434 AGAGAAGTCCCAACAGCTGTAAACTCTGGTTGCTGTGATATAAACTAAAG 483
DB 427 AGAGAAAGTCGAAGAGATTAATCTCTGGTGGAAAGTCAACAGATG 476

RESULT 10
US-09-266-910-2
Sequence 2, Application US/09266910
Patent No. 6344362
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Use of a recombinant protein as receptor of a hepatitis virus
NUMBER OF SEQUENCES: 8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,910
FILING DATE:


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; TITLE OF INVENTION: Human Elastase Inhibitor
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eileen Remold-O'Donnell, Ph.D.
; STREET: 197 Clinton Street
; CITY: Brookline
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM-compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,461A
; FILING DATE: 19910906
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/314,383
; FILING DATE: 23-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0279/7012
; INFORMATION FOR SEQ ID NO: 12
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1316 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double standard
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-07-755-461A-12

Query Match 11.0%; Score 77.4; DB 1; Length 1316;
Best Local Similarity 51.4%; Pred. No. 9.4e-14;
Matches 240; Conservative 0; Mismatches 211; Indels 16; Gaps 2;

QY 21 GCAGCTCGCGGAGAACTGGGGCTCACCGTCATGGATGCTCTATCAGAAGCAAAATGGCAC 80
DB 18 GGAGGCTCTCGGGCTGTCCGTTTTCACCATGGAGCAGCTGAGCTCAGCAAAACCCG 77

QY 81 ATTTGCATTAAACCTTTTGAAAAAGCTAGGGGAAAAACAATCTC-----AAACAATTTATTTT 136
DB 78 CTTCCCTTGGACCTTGTTCTCGGCTTGAGTGAGAACAAATCCGGCTGGAAACATCTTCAT 137

QY 137 TTTCCCATGAGCATAATCATGCGCTTGGCCATGTTTTCATGCGGGGCAAGGGAACAC 196
DB 138 CTCTCCCTTCAACATTTTCATCTGCTATGCGCATGTTTCTCGGGGACAGAGGTAACAC 197

QY 197 TCGACTCAGATGCTCTCAGGCACTTTGTTTAGTAAATCGAGGTGAAGATGGAGATAT 256
DB 198 GGCAGCAGAGCTGTCCAGACCTTCCATTTCAACAGGT-----TGAAGAGT 245

QY 257 TCATCGAGGTTTTCAGTCACTTTCTTTGTTTGTGTAATAAATAAAGTAAAG 483
DB 426 AGATGCAAGGAGAGACCATTAACCACTGGGTCAAGACAGACAGAG 472

; TITLE OF INVENTION: Human Elastase Inhibitor
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eileen Remold-O'Donnell, Ph.D.
; STREET: 197 Clinton Street
; CITY: Brookline
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM-compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755,461A
; FILING DATE: 19910906
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/314,383
; FILING DATE: 23-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0279/7012
; INFORMATION FOR SEQ ID NO: 12
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1316 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double standard
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-07-755-461A-12

Query Match 11.0%; Score 77.4; DB 1; Length 1316;
Best Local Similarity 51.4%; Pred. No. 9.4e-14;
Matches 240; Conservative 0; Mismatches 211; Indels 16; Gaps 2;

QY 21 GCAGCTCGCGGAGAACTGGGGCTCACCGTCATGGATGCTCTATCAGAAGCAAAATGGCAC 80
DB 18 GGAGGCTCTCGGGCTGTCCGTTTTCACCATGGAGCAGCTGAGCTCAGCAAAACCCG 77

QY 81 ATTTGCATTAAACCTTTTGAAAAAGCTAGGGGAAAAACAATCTC-----AAACAATTTATTTT 136
DB 78 CTTCCCTTGGACCTTGTTCTCGGCTTGAGTGAGAACAAATCCGGCTGGAAACATCTTCAT 137

QY 137 TTTCCCATGAGCATAATCATGCGCTTGGCCATGTTTTCATGCGGGGCAAGGGAACAC 196
DB 138 CTCTCCCTTCAACATTTTCATCTGCTATGCGCATGTTTCTCGGGGACAGAGGTAACAC 197

QY 197 TCGACTCAGATGCTCTCAGGCACTTTGTTTAGTAAATCGAGGTGAAGATGGAGATAT 256
DB 198 GGCAGCAGAGCTGTCCAGACCTTCCATTTCAACAGGT-----TGAAGAGT 245

QY 257 TCATCGAGGTTTTCAGTCACTTTCTTTGTTTGTGTAATAAATAAAGTAAAG 483
DB 426 AGATGCAAGGAGAGACCATTAACCACTGGGTCAAGACAGACAGAG 472

; US-08-315-831A-12
; Sequence 12: Application US/08315831A
; Patent No. 5663299
; GENERAL INFORMATION:
; APPLICANT: Remold-O'Donnell, Eileen
; TITLE OF INVENTION: Human Monocyte Elastase Inhibitor
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Ave.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,831A
; FILING DATE: September 30, 1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: C0279/7016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49...1188
; OTHER INFORMATION: /codon_start= 49
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 49...1185
; US-08-315-831A-12

Query Match 11.0%; Score 77.4; DB 1; Length 1316;
Best Local Similarity 51.4%; Pred. No. 9.4e-14;
Matches 240; Conservative 0; Mismatches 211; Indels 16; Gaps 2;

QY 21 GCAGCTCGCGGAGAACTGGGGCTCACCGTCATGGATGCTCTATCAGAAGCAAAATGGCAC 80
DB 18 GGAGGCTCTCGGGCTGTCCGTTTTCACCATGGAGCAGCTGAGCTCAGCAAAACCCG 77

QY 81 ATTTGCATTAAACCTTTTGAAAAAGCTAGGGGAAAAACAATCTC-----AAACAATTTATTTT 136
DB 78 CTTCCCTTGGACCTTGTTCTCGGCTTGAGTGAGAACAAATCCGGCTGGAAACATCTTCAT 137

QY 137 TTTCCCATGAGCATAATCATGCGCTTGGCCATGTTTTCATGCGGGGCAAGGGAACAC 196
DB 138 CTCTCCCTTCAACATTTTCATCTGCTATGCGCATGTTTCTCGGGGACAGAGGTAACAC 197

QY 197 TCGACTCAGATGCTCTCAGGCACTTTGTTTAGTAAATCGAGGTGAAGATGGAGATAT 256
DB 198 GGCAGCAGAGCTGTCCAGACCTTCCATTTCAACAGGT-----TGAAGAGT 245

QY 257 TCATCGAGGTTTTCAGTCACTTTCTTTGTTTGTGTAATAAATAAAGTAAAG 483
DB 426 AGATGCAAGGAGAGACCATTAACCACTGGGTCAAGACAGACAGAG 472
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 Db 426 AGATCAAGGAAGACCATTAACCACTGGGTCAAGGACAGACAGAAG 472

RESULT 14

US-08-662-318-12
 Sequence 12, Application US/08662318
 Patent No. 5827672

GENERAL INFORMATION:

APPLICANT: Remold-O'Donnell, Eileen
 TITLE OF INVENTION: Human Monocyte Elastase Inhibitor

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Ave.

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/662,318

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/315,831

FILING DATE: September 30, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: C0279/7016

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1316 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 49..1188

OTHER INFORMATION: /codon_start= 49

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 49..1185

US-08-662-318-12

Query Match

Best Local Similarity 11.0%; Score 77.4; DB 1; Length 1316;

Matches 240; Conservative 0; Mismatches 211; Indels 16; Gaps 2;

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 Db 18 GGAAGCTCTCGGGCGGTGCGGTTCACCATGGAGCAGCTGAGCTCAGCAAAACCCCG 77
 QY 81 ATTTCATTAAACCTTTTGAAAAAGCTAGGGGAAAAACAATC-----AAACAACCTTATTTT 136
 Db 78 CTTGCGCTTGGACCTGTCTCTGGCGTTGAGTGAGAACAAATCCGGCTGGAAACATCTTCAT 137
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 QY 317 TAGAAGTCCAAACGGGCTCTTTGGAGAAAGTCTTATGATTTCTCCTCAGAGTTTACAGA 376
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 QY 437 GAAGTCCCAACACAGCTGTAACTCTGGTGTGCTGATATAAACTAAAG 483
 Db 426 AGATCAAGGAAGACCATAAACCACTGGGTCAAGGACAGACAGAAG 472

RESULT 15

PCT-US95-12509-12

Sequence 12, Application PC/TUS9512509

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Human Monocyte Elastase Inhibitor

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Ave.

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/12509

FILING DATE: herewith

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/315,831

FILING DATE: 30 September 1994

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: C0279/7016

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1316 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

HYPOTHETICAL: NO

Wed May 28 14:44:08 2003

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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1188
; OTHER INFORMATION: /codon_start= 49
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 49..1185
; PCT-US95-12509-12

Query Match      11.0%; Score 77.4; DB 5; Length 1316;
Best Local Similarity 51.4%; Pred. No. 9.4e-14;
Matches 240; Conservative 0; Mismatches 211; Indels 16; Gaps 2;

Qy 21 GCAGCTGCGGAGAACTGGGGCTCACCGTCATGGATGCTCTATCAGAAGCAAAATGGCAC 80
Db 18 GGAGCGTCTCGGGGCTGTCGGTTTTCACCATGGAGCAGCTGAGCTCAGCAAAACACCGG 77

Qy 81 ATTGCAATTAACCTTTTGAAGAAAGCTAGGGGAAACAACTC-----AAACAACCTTATTTT 136
Db 78 CTTCGCCCTTGGACCTGTTCCTGGCGTTGAGTGAGAAACAATCCGGCTGGAAACATCTTCAT 137

Qy 137 TTTCCCATGAGCATATCATCAGCCTTGGCCATGGTTTTTCATGGGGGCAAGGGAACAC 196
Db 138 CTCTCCCTTTCAGCAATTCATCTGCTATGCGCATGGTTTTTCTGGGACCAAGAGGTAACAC 197

Qy 197 TGCAGCTCAGATGCTCAGGCACCTTTGTTTTAGTAAATCGAGGTGAAGATCGAGATAT 256
Db 198 GGCAGCACAGCTGTCCAAGACTTTCCATTTCAACACCGT-----TGAAGAGGT 245

Qy 257 TCATCGAGGTTTTTCAGTCACCTTCTGTGCAATTAACAGAACTCAGACTGAATATGTCT 316
Db 246 TCATTCAAGATTCAGAGTCTGAATGCTGATATCAACAACGTTGAGCGCTTATATCT 305

Qy 317 TAGAACTGCCAAACGGGCTCTTTGGAGAAAAGTCTTATGATTTCCCTCAGGTTTTACAGA 376
Db 306 GAAACTTGCTAATAGATTATATGAGAGAAAACCTTACAAATTCCTCCTGAGTTCTTGGT 365

Qy 377 TTCCTGTGGCAAAFTTCTACCAAGCAACGATAAACAGCTAGACTTTGTGAATGATACAGA 436
Db 366 TTCGACTCAGAAAACATATGTTGCTGACCTGGCCAGTGTGGATTTTCAGCATGCCCTCTGA 425

Qy 437 GAAGTCCACACACGTGTAACTCTCGGTTGCTGATAAAACTAAAG 483
Db 426 AGATGCAAGGAAGACCATTAACCCAGTGGGTCAAAGGACAGACAGAAG 472
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Search completed: May 21, 2003, 19:15:18
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 20:05:44 ; Search time 113 Seconds
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Title: US-09-912-628-4
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Sequence: 1 ggcacgagcttcgctctgg.....gtaaaaaaaaaaaaaa 706

Scoring table: IDENTITY NUC
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Database : Published Applications NA.*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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- 13: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	586	83.0	599	9	US-09-912-628-14
4	586	83.0	599	9	US-10-116-166-12
5	577	81.7	608	9	US-09-912-628-16
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7	462.8	65.6	943	10	US-09-728-952-86
8	251.2	35.6	1624	10	US-09-925-300-500
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11	152.6	21.6	456	10	US-09-867-701-4671
12	150.6	21.3	484	9	US-09-918-995-2112
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21	83.2	11.8	1284	10	US-09-954-456-1841	Sequence 1841, App
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24	73.6	10.4	953	7	US-08-731-566-3	Sequence 3, Appli
25	70	9.9	1950	9	US-10-091-442-30	Sequence 30, Appli
26	70	9.9	1950	10	US-09-140-719-30	Sequence 30, Appli
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43	61.8	8.8	3279	10	US-09-780-669-382	Sequence 382, App
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ALIGNMENTS

RESULT 1

US-09-912-628-4

Sequence 4, Application US/09912628

Patent No. US20020160491A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies

FILE REFERENCE: PT00192

CURRENT APPLICATION NUMBER: US/09/912,628

CURRENT FILING DATE: 2001-07-26

PRIOR APPLICATION NUMBER: PCT/US01/02484

PRIOR FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/178,769

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: PCT/US00/05082

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 706

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (635)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE

LOCATION: (655)

OTHER INFORMATION: n equals a,t,g, or c

US-09-912-628-4

Query Match 99.7%; Score 704; DB 9; Length 706;

Best Local Similarity 100.0%; Pred. No. 8.5e+219;

Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGACGAGCTTCGCTCTGGCAGCTGCGCGGAGAACTGGGGCTCACCGTCATGGATGCT 60

Qy 61 CTATCAGAACCAATGCGACATTTGCATTAAACCTTTTAAAAAGCTAGGGGAAAAAAC 120

Db 61 CTATCAGAACCAATGCGACATTTGCATTAAACCTTTTAAAAAGCTAGGGGAAAAAAC 120

10655
OTHER INFORMATION: n equals a.t.g, or c
US-10-116-166-3
Query Match 99.7%; Score 704; DB 9; Length 706;
Best Local Similarity 100.0%; Pred. No. 8.5e-219; Indels 0; Gaps 0;
Matches 706; Conservative 0; Mismatches 0;
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QY 61 CTATCAGAAGCAAAATGCAATTTGCAATTAACCTTTTGAAGAGCTAGGGGAAAAACAAC 120
DB 61 CTATCAGAAGCAAAATGCAATTTGCAATTAACCTTTTGAAGAGCTAGGGGAAAAACAAC 120
QY 121 TCAAAACAATTTATTTTCCCATGAGCATATCATCAGCTTGGCCATGGTTCATGG 180
DB 121 TCAAAACAATTTATTTTCCCATGAGCATATCATCAGCTTGGCCATGGTTCATGG 180
QY 181 GGGCAAAAGGAAACACTGCACTCAGCTCAGATGCTCAGGCACTTTTGTAGTAAATCGGAG 240
DB 181 GGGCAAAAGGAAACACTGCACTCAGCTCAGATGCTCAGGCACTTTTGTAGTAAATCGGAG 240
QY 241 GTGAAGATGGAGATATTCATCAGAGTTTTCAGTCACTTCTTGTGCAATTAACAGAACTG 300
DB 241 GTGAAGATGGAGATATTCATCAGAGTTTTCAGTCACTTCTTGTGCAATTAACAGAACTG 300
QY 301 ACACCTGGAATATGCTTTAGAACTGCCAACGGGCTCTTTGGAGAAAGTCTTATGATTTCC 360
DB 301 ACACCTGGAATATGCTTTAGAACTGCCAACGGGCTCTTTGGAGAAAGTCTTATGATTTCC 360
QY 361 TCACAGGTTTACAGATTCCTGTGCAAAATTTCTACCAAGCAACGATAAAACAGCTAGACT 420
DB 361 TCACAGGTTTACAGATTCCTGTGCAAAATTTCTACCAAGCAACGATAAAACAGCTAGACT 420
QY 421 TTGTGAATGATACAGAGAACTCCACACAGCTGTAACTCTCTGGTCTGATAAACTA 480
DB 421 TTGTGAATGATACAGAGAACTCCACACAGCTGTAACTCTCTGGTCTGATAAACTA 480
QY 481 AAGCCTGGAAATTTATTTCAAAACAAGCTGTGCAATCTGAGAGAGCCAGAAATCGCCTTT 540
DB 481 AAGCCTGGAAATTTATTTCAAAACAAGCTGTGCAATCTGAGAGAGCCAGAAATCGCCTTT 540
QY 541 CCTCTGTGTACTGCAAAAGCTGCTTTCACAGCCCTTTCAGAGCCCTTATTTCCCAAT 600
DB 541 CCTCTGTGTACTGCAAAAGCTGCTTTCACAGCCCTTTCAGAGCCCTTATTTCCCAAT 600
QY 601 GCAACTCTCTGTGACCCCGCATGCTGTGTCGTCCTCCCTCTGAGCAGAGTGTGA 660
DB 601 GCAACTCTCTGTGACCCCGCATGCTGTGTCGTCCTCCCTCTGAGCAGAGTGTGA 660
QY 661 CTAATAAACTGCGGCAATTTTCATCTGTAAAGAAAAAAGAAAAA 706
DB 661 CTAATAAACTGCGGCAATTTTCATCTGTAAAGAAAAAAGAAAAA 706
RESULT 3
US-09-912-628-14
; Sequence 14, Application US/09912628
; Patent No. US20020160491A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT001P2
; CURRENT APPLICATION NUMBER: US/09/912,628
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: PCT/US01/02484
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,769
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US00/05082
; PRIOR FILING DATE: 2000-02-29

121 TCAAAACAATTTATTTTCCCATGAGCATATCATCAGCTTGGCCATGGTTCATGG 180
121 TCAAAACAATTTATTTTCCCATGAGCATATCATCAGCTTGGCCATGGTTCATGG 180
181 GGGCAAAAGGAAACACTGCACTCAGCTCAGATGCTCAGGCACTTTTGTAGTAAATCGGAG 240
181 GGGCAAAAGGAAACACTGCACTCAGCTCAGATGCTCAGGCACTTTTGTAGTAAATCGGAG 240
241 GTGAAGATGGAGATATTCATCAGAGTTTTCAGTCACTTCTTGTGCAATTAACAGAACTG 300
241 GTGAAGATGGAGATATTCATCAGAGTTTTCAGTCACTTCTTGTGCAATTAACAGAACTG 300
301 ACACCTGGAATATGCTTTAGAACTGCCAACGGGCTCTTTGGAGAAAGTCTTATGATTTCC 360
301 ACACCTGGAATATGCTTTAGAACTGCCAACGGGCTCTTTGGAGAAAGTCTTATGATTTCC 360
361 TCACAGGTTTACAGATTCCTGTGCAAAATTTCTACCAAGCAACGATAAAACAGCTAGACT 420
361 TCACAGGTTTACAGATTCCTGTGCAAAATTTCTACCAAGCAACGATAAAACAGCTAGACT 420
421 TTGTGAATGATACAGAGAACTCCACACAGCTGTAACTCTCTGGTCTGATAAACTA 480
421 TTGTGAATGATACAGAGAACTCCACACAGCTGTAACTCTCTGGTCTGATAAACTA 480
481 AAGCCTGGAAATTTATTTCAAAACAAGCTGTGCAATCTGAGAGAGCCAGAAATCGCCTTT 540
481 AAGCCTGGAAATTTATTTCAAAACAAGCTGTGCAATCTGAGAGAGCCAGAAATCGCCTTT 540
541 CCTCTGTGTACTGCAAAAGCTGCTTTCACAGCCCTTTCAGAGCCCTTATTTCCCAAT 600
541 CCTCTGTGTACTGCAAAAGCTGCTTTCACAGCCCTTTCAGAGCCCTTATTTCCCAAT 600
601 GCAACTCTCTGTGACCCCGCATGCTGTGTCGTCCTCCCTCTGAGCAGAGTGTGA 660
601 GCAACTCTCTGTGACCCCGCATGCTGTGTCGTCCTCCCTCTGAGCAGAGTGTGA 660
661 CTAATAAACTGCGGCAATTTTCATCTGTAAAGAAAAAAGAAAAA 706
661 CTAATAAACTGCGGCAATTTTCATCTGTAAAGAAAAAAGAAAAA 706
RESULT 2
US-10-116-166-3
; Sequence 3, Application US/10116166
; Publication No. US20030040097A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT001P1
; CURRENT APPLICATION NUMBER: US/10/116,166
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/641,721
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: PCT/US00/05092
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/122,276
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 60/124,094
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/149,452
; PRIOR FILING DATE: 1999-08-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 706
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (635)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: SITE

APPLICATION NUMBER: US/09/512,628
 CURRENT FILING DATE: 2001-07-26
 PRIOR APPLICATION NUMBER: PCT/US01/02484
 PRIOR FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: PCT/US01/02484
 : PRIOR FILING DATE: 2001-01-26

;; PRIOR APPLICATION NUMBER: 60/122,276
: PRIOR FILING DATE: 1999-03-01

; PRIOR APPLICATION NUMBER: PCT/US01/02484
 : PRIOR FILING DATE: 2001-01-26


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; NAME/KEY: SITE
; LOCATION: (594)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-116-166-14

Query Match
Best Local Similarity 81.7%; Score 577; DB 9; Length 608;
Matches 598; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy 52 ATGGATGCTCTATCAGAGCAAAATGGACATTTTCGANTAAACCTTTTGAAAAAGCTAGGG 111
Db 1 ATGGATGCTCTATCAGAGCAAAATGGACATTTTCGANTAAACCTTTTGAAAAAGCTAGGG 60

Qy 112 GAAACAACTCAAACTTATTTTTC-----CCCATGAGCATATCATCAGCC 161
Db 61 GAAACAACTCAAACTTATTTTTCNNNNNNNNCCATGAGCATATCATCAGCC 120

Qy 162 TTGGCCATGTTTTCATGGGGCAAGGGAACACTGCAGCTCAGATGCTCAGGCACATT 221
Db 121 TTGGCCATGTTTTCATGGGGCAAGGGAACACTGCAGCTCAGATGCTCAGGCACATT 180

Qy 222 TGTTTTAGTAAATCGAGGTGAAGATGGAGATATTCATCGAGTTTTCAGTCACCTTCTT 281
Db 181 TGTTTTAGTAAATCGAGGTGAAGATGGAGATATTCATCGAGTTTTCAGTCACCTTCTT 240

Qy 282 GTTGCAATTAAACAGAACTGACACTGAATATGCTTTAGAACTGCCAACGGGCTCTTTGGA 341
Db 241 GTTGCAATTAAACAGAACTGACACTGAATATGCTTTAGAACTGCCAACGGGCTCTTTGGA 300

Qy 342 GAAAGTCTTATGATTTCTCTCAGAGTTTACAGATGATGCTTGAAGTCCCAACAGCTGTAACCTCC 461
Db 301 GAAAGTCTTATGATTTCTCTCAGAGTTTACAGATGATGCTTGAAGTCCCAACAGCTGTAACCTCC 420

Qy 462 TGGGTGCTGATAAAAGCTTAAAGCTTGAAGCTTGAAGTCCCAACAGCTGTAACCTCC 521
Db 421 TGGGTGCTGATAAAAGCTTAAAGCTTGAAGCTTGAAGTCCCAACAGCTGTAACCTCC 480

Qy 522 GAGCCAGGAATCGCTCTCTCTTGTGTAAGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTG 581
Db 481 GAGCCAGGAATCGCTCTCTCTTGTGTAAGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTG 540

Qy 582 GTTCACTCTATTCCTCAATCAATCTCTCTGTAAGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCT 641
Db 541 GTTCACTCTATTCCTCAATCAATCTCTCTGTAAGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCT 600

Qy 642 TCCCTGTG 649
Db 601 TCCCTGTG 608

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RESULT 7
US-09-728-952-86
; Sequence 86, Application US/09728952
; Patent No. US20020111302A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Yamazaki, Vicki
; APPLICANT: Ujwal, Manusha L.
; TITLE OF INVENTION: No. US20020111302A1el Nucleic Acids and
; FILE REFERENCE: 799
; CURRENT APPLICATION NUMBER: US/09/728,952

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; CURRENT FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: pt_FL_Genes Version 2.0
; SEQ ID NO 86
; LENGTH: 943
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(701)
US-09-728-952-86

Query Match
Best Local Similarity 65.6%; Score 462.8; DB 10; Length 943;
Matches 478; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 9 CTTTCGCTCTTCGGCAGCTGCGGGAGAACTGGGGCTCACCGTCATGGATGCTCTATCAGA 68
Db 146 CTTTCGCTCTTCGGCAGCTGCGGGAGAACTGGGGCTCACCGTCATGGATGCTCTATCAGA 205

Qy 69 AGCAAAATGGCACATTTTGCATTAAACCTTTTGAAGAAAGCTAGGGGAAAAACAACCTCAACAA 128
Db 206 AGCAAAATGGCACATTTTGCATTAAACCTTTTGAAGAAAGCTAGGGGAAAAACAACCTCAACAA 265

Qy 129 CTTATTTTTTTTCCCA-IGAGCATATCATCAGCATGCTCAGGCACTTTGTTTATGATAAACTCGAGGTGAAGA 247
Db 266 CTTATTTTTTTTCCCACTGAGCATATCATCAGCATGCTCAGGCACTTTGTTTATGATAAACTCGAGGTGAAGA 385

Qy 188 GGGAAACACTGCAGCTCAGATGCTCAGGCACTTTGTTTATGATAAACTCGAGGTGAAGA 247
Db 326 GGGAAACACTGCAGCTCAGATGCTCAGGCACTTTGTTTATGATAAACTCGAGGTGAAGA 307

Qy 248 TGGAGATATTCATCGAGGTTTTTCAGTCACCTTTGTTTGAAGTAAACAGACTGACACTGA 307
Db 386 TGGAGATATTCATCGAGGTTTTTCAGTCACCTTTGTTTGAAGTAAACAGACTGACACTGA 445

Qy 308 ATATGCTGCTAGAACTGCCAACGGGCTCTTTGGAGAAAAAGCTTTATGATTTCCTCAGCG 367
Db 446 ATATGCTGCTAGAACTGCCAACGGGCTCTTTGGAGAAAAAGCTTTATGATTTCCTCAGCG 505

Qy 368 TTTTACAGATTCCTGTCGGCAAAATCTACCAAGCAACGATAAACAGCTAGACTTTGTGAA 427
Db 506 TTTTACAGATTCCTGTCGGCAAAATCTACCAAGCAACGATAAACAGCTAGACTTTGTGAA 565

Qy 428 TGATACAGAGAGTCCCAACACGCTGTAAGTCTCTGGGTTGCTGTATAAACTAAAGCCTG 487
Db 566 TGATACAGAGAGTCCCAACACGCTGTAAGTCTCTGGGTTGCTGTATAAACTAAAGCCTG 525

Qy 488 GAAAT 493
Db 626 AATAT 631

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RESULT 8
US-09-925-300-500
; Sequence 500, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 500
; LENGTH: 1624
; TYPE: DNA

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wed May 28 14:44:08 2003

Db 184 CCATCATGATGTTCTCGCAGAACAAATGGACACCTTTTGCCTTTAAACCTTTTGAAGACGC 243
QY 107 TAGGGGAAAAACAACTCAAAACAACTTATTTTTC-CCCATGAGCATATCATCAGCCTTTGG 165
Db 244 TGGGTAAGACAACTCGAAGAAATGTGTTTTCTTCCATGAGCATGTCTCTGTGCTCTGG 303
QY 166 CCATGCTTTTCATGGGGGCAAGGAAACACATGCGAGCTCAGATGTCTCAGGCACCTTTGTT 225
Db 304 CCATGCTTACATGGGGGCAAGGAAACACCGCTGCAAGATGGCCAGATCTTTCTT 363
QY 226 TTAGTAAATTCGAGGTGAAGATGGAGATATTTTCATGAGGTTTTTCAGTCACTTTCTTTG 285
Db 364 TCAATAAAGTGGCGGT-...GGTGGAGACATCCACAGGGCTTTCAGTCTCTCTTCACCG 420
QY 286 CAATTACAGAACTGACACTGAAATATGTCTTAGAACTGCCAAAGGGCTCTTTGGGAAA 345
Db 421 AAGTGAACAAGACTGGCAGCAGTACTTGTCTTAGGGTGGCAACAGGCTCTTTGGGAAA 480
QY 346 AGTCTTATGATTTCTCTCAGAGTTTACAGATTCCTGTGGCAAAATTTCTACCAAGCAACGA 405
Db 481 AGTCTTGTGATTTCTCTCTCATCTTTTAGAGATTTCTGCGCAAAATTTCTACCAAGCAGAGA 540
QY 406 TAAACAGCTAGACTTTGTGAATGATACAGAGAGTCCACACACGTGTAAACTCTCTGGG 465
Db 541 TGGAGGAGCTTGACTTTATCAGCGCGGTAGAGAGTCCAGAAACACATAAACACCTGGG 600
QY 466 TTGCTGATAAACTAAAG 483
Db 601 TAGCTGAAAGACAGAGAAG 618

RESULT 10
US-09-974-298-94
; Sequence 94, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen Hwei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 94
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 589880CB1
US-09-974-298-94

Query Match 30.1%; Score 212.8; DB 9; Length 1476;
Best Local Similarity 73.1%; Pred. No. 1.8e-58;
Matches 320; Conservative 0; Mismatches 102; Indels 16; Gaps 3;

QY 50 TCATGGATGCTCTATCAGAAACAAATGGCACAATTCGATTAACCTTTTGAAGAACTAG 109
Db 108 TGATGGATGACCTCTGTGAAGCAATGGCACTTTTCCATCAGCTTATTTAAATAATGG 167
QY 110 GGGAAA---ACAACCTCAAACTTATTTTTC-CCCATGAGCATATCATCAGCCTTGG 165
Db 168 GGGAAAGAGGACAACTCAAGAAACGATATTTCTTCCATGAGCACTCTCTGCGCTGG 227
QY 166 CCATGCTTTTCATGGGGCAAGGAAACACACTGCGATGTCTCAGGCACCTTTGTT 225
Db 228 CCATGCTTTTCATGGGGCAAGGAAAGCACTGCGAGCCGAGATGTCCAGGCACTTTGTT 287
QY 226 TTAGTAAATTCGAGGTGAAGATGGAGATTTTCATCGAGTTTTTCAGTCACTTTCTGTTG 285
Db 288 T-----ATACAAAGACGAGAGATATTCACCGAGTTTCCAGTCTCTCTCAGTG 335

; ORGANISM: Homo sapiens
US-09-925-300-500
Query Match 35.6%; Score 251.2; DB 10; Length 1624;
Best Local Similarity 73.8%; Pred. No. 5.7e-71;
Matches 346; Conservative 1; Mismatches 119; Indels 4; Gaps 2;

QY 15 TCTTGGCAGCTGCGGGAGAACTGGGGCTCACCGTCAAGGATGCTCTATCAGAGCAAA 74
Db 277 TTCTGCTCGCTGCTCCCGCTCTGGAGTCTGCCATCATGAGATGTTCTCGCAGAGCAAA 336
QY 75 TGGCACAATTTGCATTAACCTTTTGAAGAGCTAGGGGAAACAACTCAAACTTAAT 134
Db 337 TGGCACCCTTTGCTTTAAACCTTTTGAAGACRCTGGTAAAGACAACTCGAAGAAATGTT 396
QY 135 TTTTTC-CCCATGAGCATATCATCAGCCTTTGGCCATGTTTTCATGGGGCAAGGAAA 193
Db 397 TTTTCCACCATGAGCATGCTCTGCGCTGGCCATGGTCTACATGGGGCAAGGAAA 456
QY 194 CACTGAGCTCAGATGCTCAGGCACCTTTGTTAGTAAATCGAGGTGAAGATCGAGA 253
Db 457 CACCGCTCAGAGATGGCCCAAGATCTTTCTTCAATAAAGTGGCGGT-...GCTGGAGA 513
QY 254 TATTCATCAGAGTTTTCAGTCACTTCTTGTTCGAATTAACAGAACTCAGACTGAATATGT 313
Db 514 CATCCACAGGGCTTCCAGTCTCTCTCACCAGAGTGAACAGACTGGCAGGACTT 573
QY 314 GCTTAGAAGTCCAAAGGGCTTTTGGAGAAAGTCTTATGATTTCTCAGAGTTTAC 373
Db 574 GCTTAGGATGGCCACAGGCTCTTTGGGAAAGTCTTGTGATTTCTCTCATCTTTAG 633
QY 374 AGATTCCTGTGCAAAATTTACCAAGCAACGATAAACAGCTAGACTTTGTGATGATAC 433
Db 634 AGATTCCTGCCAAATTTCTACCAAGCAGAGATGAGGAGCTTGACTTTATCAGCGCGT 693
QY 434 AGAAGAGTCCAAACAGCTGTAACTCTGGGTTCTGTATAAACTAAAG 483
Db 694 AGAAGAGTCCAGAAACACATAAACCTGGGTAGCTGAAAGACAGAG 743

RESULT 9
US-09-880-107-3027
; Sequence 3027, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3027
; LENGTH: 1465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 S69272
US-09-880-107-3027

Query Match 35.0%; Score 246.8; DB 10; Length 1465;
Best Local Similarity 75.8%; Pred. No. 1.5e-69;
Matches 332; Conservative 0; Mismatches 102; Indels 4; Gaps 2;

QY 47 CCGTCATGATGCTCTATCAGAAACAAATGGCACAATTTGCAATTAACCTTTGAAAGC 106

Qy	286	CAANTAACAGAACTGACACTGAATATGTGCTTTAGAACTGCCAACGGGCTCTTTGGAGAA	345
Db	336	AAGTTTAAACAGAACTGGCACTCAGTACTTGTCTTAGAACTGCCAAAGACTCTTTGGAGAA	395
Qy	346	AGTCCTTATGATTTCCCTCAGAGGTTTTACAGATTCCTGTGGCAAAATCTTACCAAGCAACGA	405
Db	396	AGACGTGTGATTTTCCCTTCAGACTTTTAAAGAATACTGTGAGAAGTTCTATCAGGCAGAGC	455
Qy	406	TAAACAGCTAGACTTTGTGAATGATCAGAGAAAGTCCACAAACACGTGTAAACTCCTCGG	465
Db	456	TGGAGGAGTGTGCTTGTGTAAGACACTGAAGAGTGCAGGAAGCATATAAATGACTCGG	515
Qy	466	TTGCTGATAAAACTAAAG	483
Db	516	TGCGAGAGAAGACTGAAG	533

.T 11
 US-09-867-701-4671
 ; Sequence 4671, Application US/09867701
 ; Patent No. US20020132237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aglate, Paul A.
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Harlocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/867,701
 ; CURRENT FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 10912
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4671
 ; LENGTH: 456
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-867-701-4671

Query Match	21.6%;	Score 152.6;	DB 10;	Length 456;
Best Local Similarity	67.0%;	Prod. No. 3.4e-39;		
Matches 254;	Conservative 0;	Mismatches 109;	Indels 16;	Gaps 12;
QY	41	GGCTCACGTCATGGATGCTCTATCAGAGCAAATGGCACATTTGCATTTAAACCTTTTGA	100	
DB	79	GGCCCTGTCATCGAAACCTCTTTCTAATGCAAGTGTGTACTTTTGCATACGCCCTTTAA	138	
DB	101	AAAAAGCTAGGGGAAAAACACTCAAAACAC-----TTATTTTTTCCCATGAGCATATCAT	156	
DB	139	AGATACTGTGTCAAGATAACCCCTTCGCACACAGTGTTCCTGTGAGCATCTCCT	198	
QY	157	CAGCCTTGGCCATGGTTTTTCATCGGGGCAAGGAAACACTGCAGCTCAGATGTCTCAGG	216	
DB	199	CTGCCCTGGCCATGGTTCTCTTAGGGGCAAGGAAACACCGCAACCCAGATGCCCCAGG	258	
QY	217	CACCTTGTGTTTAGTAAAAATCGGAGGTGAAGATGGAGATATTATCATCGAGTTTTTCAGTCA	276	
DB	259	CACGTCTTTTAAACA-----CAGAGAGACATTCATCGGCTTTTCAGTCCG	306	
QY	277	TTCTTGTGTGCAATTACAGAACTGACACCTGAATATGTCTTAGAACTGSCCAACGGGCTCT	336	
DB	307	TTCTACTGAAGTGAAACAAGGCTGGCACACAGTACTCTGAGAAACGGSCCAACAGGCTCT	366	
QY	337	TTGGAGAAAAAGTCTTATGATTTTCCTCACAGGTTTTTACAGATTCCTGTGGGCAAAATCTACC	396	
DB	367	TTGGAGAGAAACCTGTCAAGTTCCTCTCAAGCTTTAAGGAATCCTGTCTTCAATTTCTACC	426	
QY	397	AAGCAACGATAAAACAGCT	415	
DB	427	ATGCTGAACCTGAAGAGCT	445	

RESULT 12

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US-09-918-995-2112
; Sequence 2112, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2112
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(484)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2112

Query Match          21.3%; Score 150.6; DB 9; Length 484;
Best Local Similarity 67.0%; Pred. No. 1.6e-38;
Matches 235; Conservative 0; Mismatches 104; Indels 12; Gaps 1;

Qy      133  TTTTTPCCCATGAGCATATCATGACCTTGCCCATGGTTTTCATGGGGGCAAGGGAA 192
Db      56  TCTGTTCTCTGTGAGCATCTCTCTGCCCTGCCATGGTTCTCTAGGGGCAAGGGAA 115

Qy      193  ACACCTGAGTCTCAGATGTCTTCAGGCACATTTGTTTTAGTAAATCGGAGGTGAAGATGAG 252
Db      116  ACACCGCAACCGAGATGGCCCGACGACTGCTTTAAACA-----CAGAGGAAG 163

Qy      253  ATATTTCATCGAGGTTTTTCAGTCACTCTTGTGTGCAATTAACAGAACTGACACTGAATATG 312
Db      164  ACATTCATCGGGCTTTCCAGTCGCTTCTCACTGAAGTGAACAGGCTGGCACACAGTACC 223

Qy      313  TGCTTAGAAGTGCACACGGGCTCTTTGGAGAAAGTCTTATGATTTTCCTCACAGGTTTTTA 372
Db      224  TGCTGAGAACGGTCAACAGGCTCTTTGGAGAGAAACTTGTTCAGTTCTCTCAACGTTTA 283

Qy      373  CAGATTCTGTGGCAAAATTCTACCAAGCAACGATAAACAGCTAGACTTTTGTGAATGATA 432
Db      284  AGGAATCTCTGTCTTCAATTCTACCATGCTGAGCTGAGGAGGCTTTCTCTTATCAGAGCTG 343

Qy      433  CAGAGAGTGCACACACAGCTGTAAACTCTCTGGGTTGCTGATAAACTAAAG 483
Db      344  CAGAAGAGTGCAGGAACAACATCAACACCTGGGTCTCAAAAAGACCGAAG 394

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RESULT 13
US-10-060-036-1797
; Sequence 1797, Application US/10060036
; Publication NO. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yudu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060.036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1797
; LENGTH: 286

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Db 230 AAAAAATCTTACCAAGCAGACAGATGGAGGAGCTTGACTTTTATCAGCGCGGTAGAGAAGTCCA 171
QY 445 CAACACGTGTAAACTCTGGGTGCTCATATAAACTAAAG 483
Db 170 GAAACACATATAAACACCTGGGTAGCTGAAAAGACAGAG 132

RESULT 15

US-09-815-343-1188
; Sequence 1188, Application US/09815343
; Patent No. US20010055596A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine
; APPLICANT: Xu, Jiangchun
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.504
; CURRENT APPLICATION NUMBER: US/09/815,343
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1188
; LENGTH: 290
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-815-343-1188

Query Match 14.1%; Score 99.8; DB 10; Length 290;

Best Local Similarity 76.7%; Pred. No. 4e-22; Indels 0; Gaps 0;
Matches 122; Conservative 0; Mismatches 37;

QY 325 CCAACGGGCTCTTTGGAGAAAAGTCTTATGATTTCTCCTCAGAGTTTACAGATTCTCTGTG 384
Db 1 CCAACAGGCTCTTTGGGAAAAGTCTTGTGATTTCTCTCATCTTTTAGAGATTCTCTGCC 60
QY 385 GCAAAATTTACCAACAGCAACGATATAACAGCTAGACTTTGTGAATGATACAGAGAAGTCCA 444
Db 61 AAAAAATTTACCAACAGCAGATGGAGGAGCTTTGACTTTTATCAGCGCGGTAGAGAAGTCCA 120
QY 445 CAACACGTGTAAACTCTCTGGGTGCTGATAAACTAAAG 483
Db 121 GAAACACATATAAACCTGGGTAGCTGAAAAGACAGAG 159

Search completed: May 22, 2003, 00:20:00
Job time : 116 secs

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-1797

Query Match 20.2%; Score 142.4; DB 9; Length 286;
Best Local Similarity 73.6%; Pred. No. 5.2e-36; Indels 4; Gaps 2;
Matches 209; Conservative 0; Mismatches 71;

QY 27 GCGCGGAGAACTGGGGCTCACCGCTCATGGATGCTTATCAGAAAGCAAAATGGCACATTTGC 86
Db 6 GCTCCCGCTCTGGAGTCTGCCATCATGGATGTTCTCGCAGAAAGCAAAATGGCACATTTGC 65
QY 87 ATTAACCTTTTGAAGAAAGCTAGGGGAAACAACTAAACAACTATTTTTTC-CCCAT 145
Db 66 CTTAAACCTTTTGAAGAAAGCTAGGGTAAAGCAACTCGAAGATGTGTTTCTTCCACCAT 125
QY 146 GAGCATATCATACGCTTGGCCATGTTTTCATGGGGGCAAGGAAACAACTGCAGCTCA 205
Db 126 GAGCATGCTCTGTCCTGCGCCATGGTCTACATGGGGGCAAGGAAACAACTGCAGCTCA 185
QY 206 GATGCTCTCAGGCACTTTGTTTTAGTAAATCGGAGTGAAGATGGAGATTTTCATCGAGG 265
Db 186 GATGGCCAGACTTTCTTTCAATAAAAGTGGCGGT---GGTGGAGACATCCACCAGG 242
QY 266 TTTTCAGTCACTCTTGTGTCATTAACAGAACTGACACTGAAT 309
Db 243 CTTCCAGTCTCTTCTCCAGGAAGTGAACAGGCTGGCACCAGT 286

RESULT 14

US-10-025-380-288/c

; Sequence 288, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 290
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-288

Query Match 14.1%; Score 99.8; DB 9; Length 290;
Best Local Similarity 76.7%; Pred. No. 4e-22; Indels 0; Gaps 0;
Matches 122; Conservative 0; Mismatches 37;

QY 325 CCAACGGGCTCTTTGGAGAAAAGTCTTATGATTTCTCCTCAGAGTTTACAGATTCTCTGTG 384
Db 290 CCAACAGGCTCTTTGGGAAAAGTCTTGTGATTTCTCTCATCTTTTAGAGATTCTCTGCC 231
QY 385 GCAAAATTTACCAACAGCAACGATATAACAGCTAGACTTTGTGAATGATACAGAGAAGTCCA 444

Result No.	Query #	Query			DB	ID	Description
		Score	Match	Length			
c	1	475.4	67.3	618	14	BM696260	UI-R-DNO-
	2	404.8	57.3	557	10	AW205887	AW205887
	3	274	38.8	1150	14	BM910193	UI-H-B11-
	4	253.2	35.9	788	13	BI603219	BM510193
	5	252.6	35.8	664	13	BI603219	AGENCOURT
	6	252.6	35.8	804	12	BI669663	BI603219
						BI669663	603293204
						BG749304	602707953

Wed May 28 14:44:09 2003

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

Seq primer: M13 Reverse

FEATURES

source
1. .618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-DW0-agl-a-11-0-UI"
/clone_lib="UI-E-DW0"
/tissue_type="lens"
/dev_stage="adult"
/lab_host="PH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-DW0 is a cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
BASE COUNT 192 a 125 c 121 g 180 t
ORIGIN

Query Match 67.3%; Score 475.4; DB 14; Length 618;
Best Local Similarity 98.8%; Pred. No. 5:5e-94; Indels 0; Gaps 0;
Matches 479; Conservative 0; Mismatches 6;
9 CTTGCTCTCTGGGAGCTGCGGAGAACTGGGCTCACCGTCATGATGCTCTATCAGA 68
15 CTTGCTCTCTGGGAGCTGCGGAGAACTGGGCTCACCGTCATGATGCTCTATCAGA 74
69 AGCAATGGCACTTTCATTAACCTTTGAAAAGCTAGGGGAAACAACTCAACAA 128
75 AGCAATGGCACTTTCATTAACCTTTGAAAAGCTAGGGGAAACAACTCAACAA 134
129 CTTATTTTTCCTCCATGAGCATATCATCAGCTTGGCCATGGTTTTCATGGGGCAAAG 188
135 CTTATTTTTCCTCCATGAGCATATCATCAGCTTGGCCATGGTTTTCATGGGGCAAAG 194
189 GGAAACACTGCAGCTCAGATGTCCTCAGGACCTTTGTTTGTAGTAAATCGAGGTGAAGT 248
195 GGAAACACTGCAGCTCAGATGTCCTCAGGACCTTTGTTTGTAGTAAATCGAGGTGAAGT 254
249 GGAGATATTCATCGAGGTTTTCAGTCACCTTCTTGTGCAATTAACAGAACTGACACTGAA 308
255 GGAGATATTCATCGAGGTTTTCAGTCACCTTCTTGTGCAATTAACAGAACTGACACTGAA 314
309 TATGTCCTTAGAAGTCCCAACGGGCTTTTGGAGAAAAGTCTTATGATTTCTCAGAGT 368
315 TATGTCCTTAGAAGTCCCAACGGGCTTTTGGAGAAAAGTCTTATGATTTCTCAGAGT 374
369 TTTACAGATTCCTGTGGCAATTTCTACCAAGCAACGATAAATACAGTACAGTTTGTGAAT 428
375 TTTACAGATTCCTGTGGCAATTTCTACCAAGCAACGATAAATACAGTACAGTTTGTGAAT 434
429 GATACAGAGAGTCCCAACAGCTGTAAACTCTCTGGTTGCTGTGATAAACTAAAGCCCTGG 488
435 GATACAGAGAGTCCCAACAGCTGTAAACTCTCTGGTTGCTGTGATAAACTAAAGCTGAA 494
489 AAAAT 493
495 AATAT 499

RESULT 2
AW205887/c

LOCUS
DEFINITION
UI-H-B11-afw-d-02-0-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2723354 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AW205887
AW205887.1 GI:6505361
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 557)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CCAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1. .557
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2723354"
/clone_lib="NCI CGAP_Sub3"
/lab_host="PH10B (Life Technologies)"
/note="vector: p773-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NCI CGAP Sub3 library is a subtracted library derived from
the NCI CGAP Sub1 library, which is a subtracted library
derived from BI. BI constitutes a mixture of 21
normalized or subtracted NCI CGAP libraries: NCI CGAP_Co4
, NCI CGAP_Pr22, NCI CGAP_Pr28, NCI CGAP_Co10,
NCI CGAP_Co16, NCI CGAP_Kid5, NCI CGAP_Kid12,
NCI CGAP_Kid3, NCI CGAP_Kid11, NCI CGAP_Lym2,
NCI CGAP_Br2, NCI CGAP_Co8, NCI CGAP_CLL1, NCI CGAP_Lei2,
NCI CGAP_Brn23, NCI CGAP_Lu5, NCI CGAP_Lu24,
NCI CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI CGAP_Kid3 pool 1 LLM 3334-3337, 3682-3683,
3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775
, 1500552-1502855); NCI CGAP_Kid5 pool 1 LLM 3338-3342
, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831,
1471368-1472903, 1492104-1493255); NCI CGAP_Lu5 pool 1
LLM 3575-3582, 3851-3854 (IMAGE CloneIDs 1257096-1258631,
1520904-1522439); NCI CGAP_GC4 pool 1 LLM 3164-3167,
3716-3720, 3733-3735 (IMAGE CloneIDs 1475592-1476743); NCI CGAP_Pr22 pool 1
1469064-1470983, 1475592-1476743); NCI CGAP_Pr22 pool 1
LLM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs
945608-966759, 1101192-1101959, 1217928-1220615);
NCI CGAP_Co10 pool 1 LLM 2644-2653, 2871-2872 (IMAGE
CloneIDs 1057416-1061255, 1144584-1145351). Subtraction
was performed as previously described (Bonaldo, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery. Genome Research
6, 791-806.
TAG_LIB=NCI CGAP_Br2
TAG_TISSUE=breast
TAG_SEQ=AAACC"
BASE COUNT 168 a 98 c 98 g 193 t
ORIGIN

Query Match

57.3%; Score 404.8; DB 10; Length 557;

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FEATURES
    source
        High quality sequence stop: 523.
        Location/Qualifiers
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5442527"
                /clone_lib="NIH MGC 98"
                /tissue_type="astrocytoma grade IV, cell line"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Library constructed by Ling Hong
                in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit

```

RESULT 4	B1603219	788 bp	linear	EST 07-SEP-2001
	B1603219		mRNA	
	LOCUS	603249869F1	NIH_MGC_96	Homo sapiens cDNA clone IMAGE:5301617 5',
	DEFINITION	mRNA sequence.		
	ACCESSION	B1603219		
	VERSION	B1603219.1	GI:15496158	
	KEYWORDS	EST.		
	SOURCE	human.		
	ORGANISM	Homo sapiens		
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	TITLE	NIH-MGC http://mgc.nci.nih.gov/ .		
	JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
	COMMENT	Unpublished (1999)		
		Contact: Robert Strausberg, Ph.D.		
		Email: cgapsb-r@mail.nih.gov		
		Tissue Procurement: Miklos Palkovits, M.D., Ph.D.		
		CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki		
		Toshiyuki and Piero Carninci (RIKEN)		
		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
		DNA Sequencing by: Incyte Genomics, Inc.		
		Clone distribution: MGC clone distribution information can be		
		found through the I.M.A.G.E. Consortium/LLNL at:		
		http://image.llnl.gov		
		Plate: LLAM11763 row: j column: 18		
		High quality sequence stop: 787.		

FEATURES
source


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/dx dbref="taxon:9606"
/clone="IMAGE:5312664"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH108"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      179 a      154 c      181 g      150 t
ORIGIN

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Query Match 35.8%; Score 252.6; DB 13; Length 664;
 Best Local Similarity 73.3%; Pred. No. 2.7e-45;
 Matches 351; Conservative 0; Mismatches 124; Indels 4; Gaps 2;

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QY      6 GAGCTTCGCTCCTGGGAGAACTGGCGGAGAACTGGGGCTCACCGTCATGGATGCTCTATC 65
      28 GAGCCCTCGAGCGGAGAGAACGGCGCGCGCGGCTCGCCATCATGGATGTTCTCGC 87
      66 AGAAGCAAAATGGCAATTTGCAATTAACCTTTTGAAGAACTGGGAAACAACTCAAA 125
      88 AGAAGCAAAATGGCAATTTGCTTAAACCTTTTGAAGAACTGGGAAACAACTCGAA 147
      126 CAACCTATTTTTC-CCCATGAGCATATCATCAGCTTGGCCATGGCCATGGTTTTCATGGGGC 184
      148 GAATGTGTTTTTCTCACCACATGAGCATGTCCTGTGCGCCCTGGCCATGGTCTACATGGGGC 207
      185 AAAGGGAACACTGACGCTCAGATGCTCAGGCACTTTGTTTGTAGTAAATCGGAGTGA 244
      208 AAAGGGAACACTGACGCTGACAGATGGCCAGATCTTTTCAATAAAGTGGCGGT-- 265
      245 AGATGAGATATTCATCGAGGTTTTCAGTCAGTCTTGTGCAATTAACAGAACTGACAC 304
      266 -GGTGGAGACATCCACAGGGCTTCAGTCTCTTCTCCGGAAGTGAACAGAGTGGCAC 324
      305 TGAATATGTCTTAGAACTGCCAACGGGCTCTTTGGAGAAAAGTCTTATGATTCTCTAC 364
      325 GCAGTACTTGTAGGTTGGCCAAACAGGCTCTTTGGGAAAAGTCTTGTGATTCTCTCTC 384
      365 AGGTTTACAGATTCCTGTGGCAATTTCTACCAAGCAACGATAAAGACAGCTAGACTTGT 424
      385 ATCTTTTAGAGATTCCTGCCAAAATTTACCAAGCGAGATGGAGGAGCTTGACTTTAT 444
      425 GAATGATACAGAAAGTCCACACAGCTGTAAACTCCTGGGTGTTGTGATAAAACTAAAG 483
      445 CAGCGCGTAGAGAGTCCAGAAAACACATAAACACCTGGGTAGCTGAAAAGACAGAG 503

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RESULT 6
LOCUS    BG749304
DEFINITION 602707953F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4844629 5',
          mRNA sequence.
ACCESSION BG749304
VERSION    BG749304.1 GI:14059957
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 804)
            NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: cgabs-remail.nih.gov
            Tissue Procurement: ATCC

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BASE COUNT      220 a      175 c      205 g      187 t
ORIGIN

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Query Match 35.9%; Score 253.2; DB 13; Length 788;
 Best Local Similarity 73.3%; Pred. No. 1.9e-45;
 Matches 351; Conservative 0; Mismatches 124; Indels 4; Gaps 2;

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QY      6 GAGCTTCGCTCCTGGGAGAACTGGCGGAGAACTGGGGCTCACCGTCATGGATGCTCTATC 65
      28 GAGCCCTCGAGCGGAGAGAACGGCGCGCGGCTCGCCATCATGGATGTTCTCGC 87
      66 AGAAGCAAAATGGCAATTTGCAATTAACCTTTTGAAGAACTGGGAAACAACTCAAA 125
      88 AGAAGCAAAATGGCAATTTGCTTAAACCTTTTGAAGAACTGGGAAACAACTCGAA 147
      126 CAACCTATTTTTC-CCCATGAGCATATCATCAGCTTGGCCATGGTTTTCATGGGGC 184
      148 GAATGTGTTTTTCTCACCACATGAGCATGTCCTGTGCGCCCTGGCCATGGTCTACATGGGGC 207
      185 AAAGGGAACACTGACGCTCAGATGCTCAGGCACTTTGTTTGTAGTAAATCGGAGTGA 244
      208 AAAGGGAACACTGACGCTGACAGATGGCCAGATCTTTTCAATAAAGTGGCGGT-- 265
      245 AGATGAGATATTCATCGAGGTTTTCAGTCAGTCTTGTGCAATTAACAGAACTGACAC 304
      266 -GGTGGAGACATCCACAGGGCTTCCAGTCTCTTCTCACCAGAGTGAACAGAGTGGCAC 324
      305 TGAATATGTCTTAGAACTGCCAACGGGCTCTTTGGAGAAAAGTCTTATGATTCTCTAC 364
      325 GCAGTACTTGTAGGTTGGCCAAACAGGCTCTTTGGGAAAAGTCTTGTGATTCTCTCTC 384
      365 AGGTTTACAGATTCCTGTGGCAATTTCTACCAAGCAACGATAAAGACAGCTAGACTTGT 424
      385 ATCTTTTAGAGATTCCTGCCAAAATTTACCAAGCGAGATGGAGGAGCTTGACTTTAT 444
      425 GAATGATACAGAAAGTCCACACAGCTGTAAACTCCTGGGTGTTGTGATAAAACTAAAG 483
      445 CAGCGCGTAGAGAGTCCAGAAAACACATAAACACCTGGGTAGCTGAAAAGACAGAG 503

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RESULT 5
LOCUS    BI669663
DEFINITION 603293204F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312664 5',
          mRNA sequence.
ACCESSION BI669663
VERSION    BI669663.1 GI:15583896
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 664)
            NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: cgabs-remail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1AM11792 row: g column: 01
            High quality sequence stop: 659.
            Location/Qualifiers
            1..664
            /organism="Homo sapiens"

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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM162 row: 1 column: 14
High quality sequence stop: 683.
Location/Qualifiers
1. .804
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:484629"
/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcORI; cDNA made by oligo-dT priming. Directionally
cloned into EcORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. "
BASE COUNT 229 a 187 c 205 g 183 t

FEATURES
source

Query Match 35.8%; Score 252.6; DB 12; Length 804;
Best Local Similarity 73.3%; Pred. No. 2.5e-45;
Matches 351; Conservative 0; Mismatches 124; Indels 4; Gaps 2;
QY 6 GAGCTTCGCTCCTGGGAGCTGCGGAGAACTGGGCTACCGTCATGGATGCTCTATC 65
Db 10 GAGCTTCGCGGAGAGAACGGCGCGCGGCTGCGCATCATGATGTTCTCGC 69
QY 66 AGAAGCAAAATGGCAATTTGATTAACCTTTTGAAGAACTAGGGGAAACAACTCAA 125
Db 70 AGAAGCAAAATGGCACTTTGCTTAAACCTTTTGAAGAACTAGGGTAAAGCAACTCGAA 129
QY 126 CAATCTATTTTTTC-CCCATGAGCATATCATCAGCCCTTGGCCATGTTTTCATGGGGC 184
Db 130 GAATGTGTGTTTTCTCACCCATGAGCATGTCTGTGCGCTGCGCATGCTTACATGGGGC 189
QY 185 AAAGGAAACACTCAGCTCAGATGTCTCAGGACATTTGTTTAAATCGAGGTGA 244
Db 190 AAAGGAAACACTCAGCTCAGATGTCTCAGGACATTTTCTTCAATAAAGTGGCGT-- 247
QY 245 AGATGAGATATTTCATCGAGGTTTTTCAGTCACATCTTGTGCAATTAACAGACTGCAC 304
Db 248 -GGTGGAGACATCCACAGGCTTCCAGTCTCTTCTCAGCAAGTGAACAGACTGGCAC 306
QY 305 TGAATATGCTGTAGAACTCCAAACGGGCTCTTTGGAGAAAGTCTTATGATTTCTCTAC 364
Db 307 GCAGTACTGCTTAGGATGGCCAAACAGGCTCTTTGGGAAAGTCTTGTGATTTCTCTC 366
QY 365 AGGTTTTACAGATTTCTGTGGCAAAATCTACCAAGCAACGATAAACACTGACTTTGT 424
Db 367 ATCTTTTAGAGATTCCTGCCAAAATTTCTACCAAGCAGAGATGGAGAGCTTGACTTTAT 426
QY 425 GAATGATACAGAGAGTCCCAACACAGCTGTAAACTCTCGGTGCTGATATAAACTAAAG 483
Db 427 CAGCGCGGTAGAGAGTCCAGAAACACATTAACACTCGGTAGCTGAAAGACAGAG 485

RESULT 7
BO681973
LOCUS
DEFINITION
AGENCOURT_9212433 NIH_MGC_112 Homo sapiens CDNA clone IMAGE:6260725
5', mRNA sequence.
ACCESSION
BO681973
VERSION
BO681973.1 GI:21794652
KEYWORDS
EST.
SOURCE
human.

ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 905)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: c9apbs@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2420 row: e column: 14
High quality sequence stop: 649.
Location/Qualifiers
1. .905
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6260725"
/clone_lib="NIH_MGC_112"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcORI; cDNA made by oligo-dT priming. Directionally cloned
into EcORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

FEATURES
source

BASE COUNT
ORIGIN

261 a 196 c 246 g 201 t 1 others
Query Match 35.8%; Score 252.6; DB 14; Length 905;
Best Local Similarity 73.3%; Pred. No. 2.5e-45;
Matches 351; Conservative 0; Mismatches 124; Indels 4; Gaps 2;
QY 6 GAGCTTCGCTCCTGGGAGCTGCGGAGAACTGGGCTACCGTCATGGATGCTCTATC 65
Db 45 GAGCTTCGCGGAGAGAACGGCGCGCGGCTGCGCATCATGATGTTCTCGC 104
QY 66 AGAAGCAAAATGGCAATTTGATTAACCTTTTGAAGAACTAGGGGAAACAACTCAA 125
Db 105 AGAAGCAAAATGGCACTTTGCTTAAACCTTTTGAAGAACTAGGGTAAAGCAACTCGAA 164
QY 126 CAATCTATTTTTTC-CCCATGAGCATATCATCAGCCCTTGGCCATGTTTTCATGGGGC 184
Db 165 GAATGTGTTTTCTCACCCATGAGCATGTCTGTGCGCTGCGCATGCTTACATGGGGC 224
QY 195 AAAGGAAACACTCAGCTCAGATGTCTCAGGACATTTGTTTAAATCGAGGTGA 244
Db 225 AAAGGAAACACTCAGCTCAGATGTCTCAGGACATTTTCTTCAATAAAGTGGCGT-- 282
QY 245 AGATGAGATATTTCATCGAGGTTTTTCAGTCACATCTTGTGCAATTAACAGACTGCAC 304
Db 283 -GGTGGAGACATCCACAGGCTTCCAGTCTCTTCTCAGCAAGTGAACAGACTGGCAC 341
QY 305 TGAATATGCTGTAGAACTCCAAACGGGCTCTTTGGAGAAAGTCTTATGATTTCTCTAC 364
Db 342 GCAGTACTGCTTAGGATGGCCAAACAGGCTCTTTGGGAAAGTCTTGTGATTTCTCTC 401
QY 365 AGGTTTTACAGATTTCTGTGGCAAAATCTACCAAGCAACGATAAACACTGACTTTGT 424
Db 402 ATCTTTTAGAGATTCCTGCCAAAATTTCTACCAAGCAGAGATGGAGAGCTTGACTTTAT 461
QY 425 GAATGATACAGAGAGTCCCAACACAGCTGTAAACTCTCGGTGCTGATATAAACTAAAG 483
Db 462 CAGCGCGGTAGAGAGTCCAGAAACACATTAACACTCGGTAGCTGAAAGACAGAG 520

QY 372 ACAGATTCTGTGGCAAAATTTACCAAGCAACATATAAAACAGCTAGACTTTGTGAATGAT 431
 Db 379 AAGATTCTCTGCCCAAAATTTACCAAGCGAGATGGAAGCTGGACTTTGTCAACACG 438
 QY 432 ACAGAGAAAGTCCCAACACAGCTGTAAATCTCTGGTTCTGTATATAAACTAAG 483
 Db 439 ACAGAGGAGTCCCGGAACACATAAAACACCTGGGTAGCCGAGAGACAGAAG 490

RESULT 9
 BE543971 536 bp mRNA linear EST 09-AUG-2000
 LOCUS 601070485F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456500 5',
 DEFINITION mRNA sequence.
 ACCESSION BE543971
 VERSION BE543971.1 GI:9772616
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 536)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: LLAM8444 row: j column: 21
 High quality sequence stop: 534.
 Location/Qualifiers
 1..536
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:3456500"
 /clone_lib="NIH MGC 12"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1; NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."
 BASE COUNT 132 a 143 c 135 g 126 t
 ORIGIN

Query Match 35.6%; Score 251.6; DB 10; Length 536;
 Best Local Similarity 73.8%; Pred. No. 4.7e-45;
 Matches 347; Conservative 0; Mismatches 119; Indels 4; Gaps 2;
 QY 15 TCTGGGAGCTCGCGGAGAACTGGGCTCCCGTCACTGGATGCTCTATCAGAACAAA 74
 Db 61 TTCTGCTCGCTCGCTCCCGCTCTGGAGTCTGCATCATGGATGTTCTCGAGAACAAA 120
 QY 75 TGGCACATTTGCAATTAACCTTTTGAAGAGCTAGGGGAAACAACTCAACAACTTATT 134
 Db 121 TGGACCTTTGCTTAAACCTTTTGAAGAGCTGGGTGGAAGCACTCGAAGATGTGT 180
 QY 135 TTTTTC-CCCATGAGCATATCATCAGCTTGGCCATGGTTTCATGGGGCAAGGAAA 193
 Db 181 TTTTCTACCCATGAGCATGTCTGTGCTGCTGGCCATGGTCTACATGGGGCAAGGAAA 240
 QY 194 CACTGAGCTCAGATGTCTCAGGACCTTTCTTTTAGTAAATCGAGGTGAAGATGAGA 253
 Db 241 CACCGCTGCACAGATGGCCCGAGATCTTCTTCAATAAAGTGGCGGT---GGTGA 297
 QY 254 TATTCTCAGAGGTTTTCAGTCACTTCTTGTGCAATTAACAGAACTGACACTGAATGT 313

LOCUS BG894979 595 bp mRNA linear EST 05-JUN-2001
 DEFINITION 355775 MARC 1PTG Sus scrofa cDNA 5', mRNA sequence.
 ACCESSION BG894979
 VERSION BG894979.1 GI:14305220
 KEYWORDS EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 REFERENCE 1 (bases 1 to 595)
 AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
 Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
 and Keele, J.W.
 TITLE Design and use of two pooled tissue normalized cDNA libraries for
 EST discovery in swine
 JOURNAL Unpublished (2000)
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCAGTCAAGCAGC
 Plate: 120 row: P column: 8
 Seq primer: ATTAGGTGACACTATAG.
 Location/Qualifiers
 1..595
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="MARC 1PTG"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site: 1; NotI; Site: 2: SalI;
 Library made from pooled tissue from day 11, 13, 15, 20,
 and 30 embryos."
 BASE COUNT 157 a 173 c 136 g 129 t
 ORIGIN

Query Match 35.7%; Score 252; DB 12; Length 595;
 Best Local Similarity 72.2%; Pred. No. 3.7e-45;
 Matches 341; Conservative 0; Mismatches 130; Indels 1; Gaps 1;
 Db 12 CGCTCTGGCAGCTCGCGGAGAACTGGGCTCACCGTCACTGATGCTCTATCAGAAAGC 71
 QY 20 CGCCGCCCGCAGCGTCCGGTCCGCTCGGACTTCCCGTCACTGATGCTCTGTGGAGGC 79
 Db 72 AATGGCAGCTTTGCTTAAACCTTTTGAAGAGCTAGGGGAAACAACTCAAACTT 131
 QY 80 AATGGCAGCTTTGCTTAAACCTTTTGAAGAGCTAGGGGAAACAACTCAAACTT 138
 QY 132 ATTTTTCCTCCATGAGCATATCATCAGCTTGGCCATGGTTTCATGGGGCAAGGGA 191
 Db 139 TTTTCTCACCCTAGAGCTCTCTCCAGCTGGCCATGGTCTTTATGGGGCAGCAGGC 198
 QY 192 AACCTGAGCTCAGATGTCTCAGGACCTTTCTTTTAGTAAATCGAGGTGAAGATGGA 251
 Db 199 AACACCGCAACTCAGATGTCTCAGGACCTTTCTTAAGCAAAAGCAGCAGAAAGTGA 258
 QY 252 GATATTTCAGAGGTTTTCAGTCACTTTCTTTGTTGCAATTAACAGAACTGACACTGAAT 311
 Db 259 GATGTCCACAGGTTTTCAGAACTTCTCACCAGAGTCAACAGGACTGGCACAGTAC 318
 QY 312 GTGCTTAGACTGCCAAGGGCTTTTGGAGAAAGTCTTATGATTCTCTCAGAGTTT 371
 Db 319 TTGCTCAGAAACCGCCCAACAGGCTCTTCGGAGAGAGTCTTACGGTTTCTCTCCATCTTC 378

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Db      298 CATCCACAGGCTCTCCAGTCTCTCTCACCAGAGTGAACAGACTGGCAGCAGTACTT 357
Qy      314 GCTTAGAAGTGCACCAAGGCTCTTTGGAGAAAGTCTTATGATTTCTCAGAGTTTATC 373
Db      358 GCTTAGAGTGGCAACAGGCTCTTTGGGAAAGTCTTTGTGATTTCTCTCATCTTTTGG 417
Qy      374 AGATTCTGTGGCAAAATTTACCAAGCAACGATATAAAGCAGCTAGACTTTGTGATGATAC 433
Db      418 AGATTCTGTGGCAAAATTTACCAAGCAACGATATAAAGCAGCTAGACTTTGTGATGATAC 477
Qy      434 AGAGAAGTCCCAACAGCTGTAAACTCTCTGGTGTCTGATATAAACTAAAG 483
Db      478 AGAGAAGTCCCAACAGCTGTAAACTCTCTGGTGTCTGATATAAACTAAAG 527

RESULT 10
LOCUS      BI222640                818 bp      mRNA      linear      EST 11-JUL-2001
DEFINITION 602940135F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5103344 5',
mRNA sequence.
ACCESSION  BI222640
VERSION     BI222640.1 GI:14676084
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        NIH-MGC http://mgc.nci.nih.gov/
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11249 row: e column: 09
High quality sequence stop: 764.
FEATURES             Location/Qualifiers
     source           1..818
     organism="Homo sapiens"
     db_xref="taxon:9606"
     clone="IMAGE:5103344"
     clone_lib="NIH_MGC_12"
     tissue_type="cervical carcinoma cell line"
     lab_host="DH10B"
     notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
     Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
     Average insert size 1.4 kb. Library prepared by Life
     Technologies."
BASE COUNT          191 a 224 c 221 g 182 t
ORIGIN
Query Match          35.6%; Score 251.6; DB 13; Length 818;
Best Local Similarity 73.8%; Pred. No. 4.2e-45;
Matches 347; Conservative 0; Mismatches 119; Indels 4; Gaps 2;
Qy      15 TCTTGGCAGCTCGCGGAGAACTGGGGCTACCGTCATCGATGCTCTATCAGAGCAAA 74
Db      158 TTCTGCTCGCTCCCCGCTCTGGAGTCTGCCATCATGATGTTCTCGCAGAGCAAA 217
Qy      75 TGSCACATTGGCATTAACCTTTTGAAGAAAGCTAGGGGAAACAACTCAAACTTATT 134
Db      218 TGSCACCTTTGGCTTAAACCTTTTGAAGAAAGCTGGGTAAGAACTCGAAGATGTGT 277
Qy      135 TTTTTC-CCCATGAGCATATCATGACCTTTGGCCATGGTTTTCATGGGGCAAGGGAAA 193
Db      278 TTTCTCACCCTCAGCATGTCTGTGCTGCTGCGCCATGTGTCTACATGGGGCAAGGGAAA 337

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Qy      194 CACTGCAGCTCAGATGTCTCAGGCACCTTTGTTTAAATCGGAGGTGAAGATGAGA 253
Db      338 CACCGTGCACAGATGGCCAGATACTTTCTTTCAATAAAGTGGCGGT---GGTGGAGA 394
Qy      254 TATTTCATCAGAGTTTTCAGTCACTTCTTGTGCAATTACAGAACTGACACTGAATATGT 313
Db      395 CATCCACAGGCTTCCAGTCTCTTCTCACCCAGAGTGAACAGACTGGCAGCAGTACTT 454
Qy      314 GCTTAGAAGTGCACCAAGGCTCTTTGGAGAAAGTCTTATGATTTCTCAGAGTTTATC 373
Db      455 GCTTAGAGTGGCCCAACAGGCTCTTTGGGAAAGTCTTGTGATTTCTCTCATCTTTTGG 514
Qy      374 AGATTCTGTGGCAAAATTTACCAAGCAACGATATAAAGCAGCTAGACTTTGTGATGATAC 433
Db      515 AGATTCTGTGGCAAAATTTACCAAGCAACGATATAAAGCAGCTAGACTTTGTGATGATAC 574
Qy      434 AGAGAAGTCCCAACAGCTGTAAACTCTCTGGTGTCTGATATAAACTAAAG 483
Db      575 AGAGAAGTCCCAACAGCTGTAAACTCTCTGGTGTCTGATATAAACTAAAG 624

RESULT 11
LOCUS      BG108578                875 bp      mRNA      linear      EST 30-JAN-2001
DEFINITION 602278558F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4366047 5',
mRNA sequence.
ACCESSION  BG108578
VERSION     BG108578.1 GI:12602424
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        NIH-MGC http://mgc.nci.nih.gov/
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10016 row: d column: 16
High quality sequence stop: 704.
FEATURES             Location/Qualifiers
     source           1..875
     organism="Homo sapiens"
     db_xref="taxon:9606"
     clone="IMAGE:4366047"
     clone_lib="NIH_MGC_86"
     tissue_type="osteosarcoma, cell line"
     lab_host="DH10B (phage-resistant)"
     notes="Organ: bone; Vector: pCMV-SPORT6; Site 1: NotI;
     Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
     Average insert size 1.53 kb. Library enriched for
     full-length clones and constructed by Life Technologies.
     Note: this is a NIH_MGC Library."
BASE COUNT          224 a 216 c 225 g 210 t
ORIGIN
Query Match          35.6%; Score 251.6; DB 12; Length 875;
Best Local Similarity 73.8%; Pred. No. 4.1e-45;
Matches 347; Conservative 0; Mismatches 119; Indels 4; Gaps 2;
Qy      15 TCCTGGCAGCTCGCGGAGAACTGGGGCTCAGGTCATCGATGCTCTATCAGAGCAAA 74
Db      76 TTCTGCTCGCTCCCCGCTCTGGAGTCTGCCATCATGATGTTCTCGCAGAGCAAA 135

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QY 75 TGGCACAATTTGGCATTAAACCTTTTGAAGAGCTAGGGGAAACAACTCAACAACTTATT 134
 Db 136 TGGCACCCTTTGGCTTAAACCTTTTGAAGAGCTAGGGGAAACAACTCAACAACTTATT 195
 QY 135 TTTTTC-CCCATGAGCATATCATCAGCTTTGGCCATGGTTTTCATGGGGGCAAGGGAAA 193
 Db 196 TTTCTCACCACATAGAGATGCTCTGTGCTTGGCCATGGTTTTCATGGGGGCAAGGGAAA 255
 QY 194 CACTGCAGCTCAGATGCTCAGGCACTTTTGTAGTAAATCGGAGTGAAGATGGAGA 253
 Db 256 CACCGTGCACAGATGGCCAGACTTTCTTCAATAAAAGTGGCGGT---GGTGGAGA 312
 QY 254 TATTCATCGAGTTTTCAGTCACTTCTTGTGCAATTAACAGAACTGACCTGAATATGT 313
 Db 313 CATCCACCGGGCTTCCAGTCTCTTCTCACCGAAGTGAACAGACTGGCAGCAGTACTT 372
 QY 314 GCTTAGACTGCCAAGCGGCTTTTGGAGAAAGTCTTATGATTTTCTCAGAGTTTATAC 373
 Db 373 GCTTAGAGTGGCCAAACAGGCTTTTGGGAAAGTCTTGTGATTTCTCTCATCTTTTAG 432
 QY 374 AGATTCCTGTGGCAAAATTTACCAAGCAACGATATAAAGCTAGACTTTGTGAATATAC 433
 Db 433 AGATTCCTGCCAAAATTTACCAAGCAGAGATGGAGGAGCTTGACTTTATCAGCGCGT 492
 QY 434 AGAGAAGTCCAAACAGCTGTAACTCTCTGGGTTGCTGATAAACTAAAG 483
 Db 493 AGAGAAGTCCAAACACATACACCTGGGTAGCTGAAAGACAGAG 542

RESULT 12
 BM461676 880 bp mRNA linear EST 05-FEB-2002
 LOCUS AGENCOURT 6418371 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5533721
 DEFINITION 5', mRNA sequence.

ACCESSION BM461676
 VERSION BM461676.1 GI:18510716
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 880)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12219 row: a column: 18
 High quality sequence stop: 659.
 Location/Qualifiers
 1..880
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 /db_xref="taxon:9606"
 /clone="IMAGE:5533721"
 /clone_lib="NIH MGC 71"
 /tissue_type="leiomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: Not I; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb."

BASE COUNT 239 a 206 c 226 g 209 t
 ORIGIN
 Query Match 35.6%; Score 251.6; DB 13; Length 880;
 Best Local Similarity 73.8%; Pred. No. 4.1e-45;
 Matches 347; Conservative 0; Mismatches 119; Indels 4; Gaps 2;

QY 15 TCCTGGCAGCTGCGGGAGAACTGGGGCTCACCGTCATGATCTCTATCAGAAGCAAA 74
 Db 74 TTTCTGCTGGCTCGCTCCCGCTCTGGAGTCTGCCATCATGATGTCTTCGAGAAGCAAA 133
 QY 75 TGGCACAATTTGCATTAAACCTTTTGAAGAGCTAGGGGAAACAACTCAACAACTTATT 134
 Db 134 TGGCACCCTTTGGCTTAAACCTTTTGAAGAGCTAGGGGAAACAACTCAACAACTTATT 193
 QY 135 TTTTTC-CCCATGAGCATATCATCAGCTTTGGCCATGGTTTTCATGGGGGCAAGGGAAA 193
 Db 194 TTTCTCACCACATAGAGATGCTCTGTGCTTGGCCATGGTTTTCATGGGGGCAAGGGAAA 253
 QY 194 CACTGCAGCTCAGATGCTCAGGCACTTTTGTAGTAAATCGGAGTGAAGATGGAGA 253
 Db 254 CACCGTGCACAGATGGCCAGACTTTCTTCAATAAAAGTGGCGGT---GGTGGAGA 310
 QY 254 TATTCATCGAGTTTTCAGTCACTTCTTGTGCAATTAACAGAACTGACCTGAATATGT 313
 Db 313 CATCCACCGGGCTTCCAGTCTCTTCTCACCGAAGTGAACAGACTGGCAGCAGTACTT 370
 QY 314 GCTTAGACTGCCAAGCGGCTTTTGGAGAAAGTCTTATGATTTTCTCAGAGTTTATAC 373
 Db 373 GCTTAGAGTGGCCAAACAGGCTTTTGGGAAAGTCTTGTGATTTCTCTCATCTTTTAG 430
 QY 374 AGATTCCTGTGGCAAAATTTACCAAGCAACGATATAAAGCTAGACTTTGTGAATATAC 433
 Db 431 AGATTCCTGCCAAAATTTACCAAGCAGAGATGGAGGAGCTTGACTTTATCAGCGCGT 490
 QY 434 AGAGAAGTCCAAACAGCTGTAACTCTCTGGGTTGCTGATAAACTAAAG 483
 Db 491 AGAGAAGTCCAAACACATACACCTGGGTAGCTGAAAGACAGAG 540

RESULT 13
 BQ949817 927 bp mRNA linear EST 21-AUG-2002
 LOCUS AGENCOURT 8744336 Lupski_sciatic_nerve Homo sapiens cDNA clone
 DEFINITION IMAGE:6205988 5', mRNA sequence.

ACCESSION BQ949817
 VERSION BQ949817
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 927)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM13629 row: 1 column: 21
 High quality sequence stop: 729.
 Location/Qualifiers
 1..927
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6205988"
 /clone_lib="Lupski_sciatic_nerve"
 /sex="male"
 /tissue_type="sciatic nerve"
 /dev_stage="adult, 70 yr"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1: Not I; Site 2: SalI; cDNA made by oligo-dT priming."

FEATURES
 source
 1..927
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6205988"
 /clone_lib="Lupski_sciatic_nerve"
 /sex="male"
 /tissue_type="sciatic nerve"
 /dev_stage="adult, 70 yr"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1: Not I; Site 2: SalI; cDNA made by oligo-dT priming."

Directionally cloned using the following adaptors:
 5'-GACTACCGGCGCG-3' and
 1 kb for average insert length 1.87 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupsaki, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."

BASE COUNT 253 a 208 c 244 g 220 t 2 others
 ORIGIN

Query Match 35.6%; Score 251.6; DB 14; Length 927;
 Best Local Similarity 73.8%; Pred. No. 4e-45;
 Matches 347; Conservative 0; Mismatches 119; Indels 4; Gaps 2;

QY 15 TCCTGGGAGCTGCGGAGAACTGGGGCTCACCGTCATGGATGCTCTATCAGAAGCAAA 74
 |||||
 58 TTCTGCTGGCTCGCTCCCGCTCTGGAGTCTGCCATCATGATGTTCTCGCAGAGCAAA 117
 |||||
 75 TGGCATTTCGATTAACCTTTTGAAGAGCTAGGGGAAACAACTCAAACTTATT 134
 |||||
 118 TGGCACCTTTGGCTTTAAACCTTTTGAAGAGCTGGGTAAAGACAACTCGAAGATGTGT 177
 |||||
 135 TTTTTC-CCCATGAGCATATCATAGCCTTGCCATGCTTTTCATGGGGCAAGGAAA 193
 |||||
 178 TTTCTACCATGAGCATGCTCTGTGCCCTGGCCATGCTTACATGGGGGCAAGGAAA 237
 |||||
 194 CACTGCAGCTCAGATGCTCAGGCACCTTTGTTTGTAGTAAATCGAGGTGAAGATGAGA 253
 |||||
 238 CACCGCTGCACAGATGGCCAGATATCTTTCAATAAAGTGGCGT---GGTGGAGA 294
 |||||
 254 TATTATCGAGGTTTTCAGTCACCTCTGTTGCAATTAACAGACTGACACTGAATATGT 313
 |||||
 295 CATCCACAGGCTTCCAGTCTCTTCACCCGAAGTGAACAGACTGCGCAGCAGTACTT 354
 |||||
 314 GCTTAGAACTGCCAACGGCTCTTTGGAGAAAGCTTTATGATTTCTCAGAGTTTAC 373
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 355 GCTTAGATGCGCAACAGGCTCTTTGGGAAAGCTTTGATTTCTCTCATCTTTTAG 414
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 374 AGATTCCTGCGCAATTTCTACCAAGCAACGATAAAACAGTACGTTTGTGAATGATAC 433
 |||||
 415 AGATTCCTGCGCAATTTCTACCAAGCAGAGATGGAGGCTTGACTTTATCAGCGCGT 474
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 434 AGAGAAGTCCACACACGTGTAAACTCTCGGTTGCTGATAAACTAAAG 483
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 475 AGAGAAGTCCAGAAACACATAAACCTCGGTAGCTGAAAGACAGAAAG 524
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RESULT 14
 B1822888
 LOCUS 603040326F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5181246 5',
 DEFINITION mRNA sequence.
 ACCESSION B1822888
 VERSION B1822888.1 GI:15934438
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC <http://mhc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-f@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM11452 row: c column: 07
 High quality sequence stop: 797.

FEATURES
 source

Location/Qualifiers
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 /clone="IMAGE:5181246"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /notes="Organ: pooled brain, lung, testis; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH MGC Library."

BASE COUNT 223 a 256 c 260 g 218 t
 ORIGIN

Query Match 35.6%; Score 251.6; DB 13; Length 957;
 Best Local Similarity 73.8%; Pred. No. 4e-45;
 Matches 347; Conservative 0; Mismatches 119; Indels 4; Gaps 2;

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 203 TTTCTGCTCGCTCGCTCCCGCTCTGGAGTCTGCCATCATGATGTTCTCGCAGAGCAAA 262
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 314 GCTTAGAACTGCCAACGGCTCTTTGGAGAAAGTCTTATGATTTCTCAGAGTTTAC 373
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RESULT 15
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 LOCUS 603040326F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5761538
 DEFINITION 5', mRNA sequence.
 ACCESSION BQ072385
 VERSION BQ072385.1 GI:19901431
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC <http://mhc.nci.nih.gov/>.

Wed May 28 14:44:09 2003

us-09-912-628-4.rst

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM2810 row: f column: 03
High quality sequence stop: 666.
Location/Qualifiers
1. .991
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/db_xref="taxon:9606"
/clone="IMAGE:5761538"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH MGC Library."

FEATURES
source

BASE COUNT 275 a 230 c 255 g 231 t
ORIGIN
Query Match 35.6%; Score 251.6; DB 14; Length 991;
Best Local Similarity 73.8%; Pred. No. 4e-45;
Matches 347; Conservative 0; Mismatches 119; Indels 4; Gaps 2;
QY 15 TCCTGGGCGAGCTGGCGGAGAACTGGGGCTCACCGTCATGGTCTCTATCAGAAGCAA 74
Db 80 TTCTGCTCGCTCGCTCCCGCTCTGGAGTCGGCCATCATGATGTTCTCGAGAGCAA 139
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QY 254 TATTCATCGAGGTTTCAGTCACTTTGTTGTCATTAACAGAACTGACTGAATATGT 313
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Db 377 GCTTAGAAGTCCACAGGGCTTTGGGAAAGTCTTGTGATTTCTCTCATCTTTAG 436
QY 374 AGATTCTCTGGCAATTTACCAAGCAACGATAAAGAGCTAGACTTTGTGAATGATAC 433
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Db 497 AGAGAAGTCCACAGAAACACATAAACACCTGGGTAGTGTAAAGACAGAAAG 546

GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2003, 10:19:06 ; Search time 76 seconds
(without alignments)
376.959 Million cell updates/sec

Title: US-09-912-628-7

Perfect score: 1145

Sequence: 1 HELRSWAARRTGAHRHGS.....SIPKNSPVTGHWXPPSL 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1143	99.8	215	21	AA080776
2	1143	99.8	215	22	AA014914
3	896	78.3	199	21	AA080783
4	896	78.3	199	22	AA014921
5	893	78.0	202	21	AA080784
6	893	78.0	202	22	AA014922
7	885.5	77.3	201	21	AA080777
8	885.5	77.3	201	22	AA014915
9	600	52.4	170	23	ABG66743
10	404.5	35.3	319	22	AAU02922

11	404.5	35.3	372	22	AAU02963	Angiotensin conver
12	404.5	35.3	400	22	AAU02962	Angiotensin conver
13	403.5	35.2	204	22	AAU02974	Angiotensin conver
14	403.5	35.2	376	22	AA059176	Thrombin inhibitor
15	403.5	35.2	376	22	AA011125	Human thrombin inh
16	403.5	35.2	389	22	AAU02973	Angiotensin conver
17	403.5	35.2	459	21	AA056862	Human prostate can
18	399	34.8	156	22	AAU02975	Angiotensin conver
19	392.5	34.3	374	17	AA099253	Cytolaemic antipr
20	392.5	34.3	374	21	AA055840	Human cytoplaemic
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23	320	27.9	376	21	AA055841	Human cytoplaemic
24	278	24.3	390	18	AA015241	Psoriasisatin type
25	272	23.8	390	18	AA015242	Psoriasisatin type
26	272	23.8	390	20	AA015242	Human SCCA2 protei
27	272	23.8	390	20	AA015242	Human SCCA2 protei
28	266	23.2	390	13	AA025276	Human squamous cel
29	266	23.2	390	20	AA025276	Human squamous cel
30	266	23.2	390	20	AA025276	Human squamous cel
31	266	23.2	390	20	AA025276	Human squamous cel
32	266	23.2	390	20	AA025276	Human squamous cel
33	246	21.5	382	12	AA012144	Plasminogen activa
34	240	21.0	379	17	AA094367	Human elastase inh
35	240	21.0	437	21	AA043755	Human cancer asoc
36	239	20.9	379	16	AA064159	Human elastase inh
37	235	20.5	188	22	AAU02923	Angiotensin conver
38	232	20.3	392	12	AA012143	Plasminogen activa
39	229	20.0	41	21	AA080782	Human serine prote
40	229	20.0	41	22	AA014920	Human serine prote
41	225.5	19.7	438	12	AA011353	ProB-PAI-2 with al
42	224	19.6	224	22	AA072660	Human headpin (for
43	224	19.6	316	20	AA028644	Human serine prote
44	224	19.6	391	20	AA041029	Human lung tumor a
45	224	19.6	391	20	AA025926	Human hurpin prote

ALIGNMENTS

RESULT 1

AA080776

ID AAB08776 standard; Protein; 215 AA.

XX

AA080776;

XX

DT 02-JAN-2001 (first entry)

XX

DE Amino acid sequence of a human serpin polypeptide.

XX

Human; serpin; serine protease inhibitor; autoimmune disease; neoplasia; rheumatoid arthritis; hyperproliferative disorder; cerebral ischemia; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; angiosclerosis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; epithelial cell proliferation; skin aging; sunburn; wound healing; organ transplantation; chemotaxis; food additive; food preservative.

OS Homo sapiens.

XX

XX

FH Key Location/Qualifiers

FT Misc-difference 211

/note= "any L-amino acid which is encoded by TGN"

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Ruben SM, Ni J;
XX DR WPI; 2000-579284/54.
XX DR N-PSDB; AAA64690.
XX XX Novel human serine protease inhibitor superfamily of proteins useful
XX PT for diagnosing, treating, preventing and/or prognosing disorders
XX PT related to the Serpin polypeptides
XX XX Claim 12; Page 204; 215pp; English.
XX PS The present sequence represents a human serpin polypeptide. Serpin is
XX CC a member of the serine protease inhibitor superfamily of polypeptides.
XX CC The serpin polynucleotides and polypeptides are used to prevent, treat
XX CC or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
XX CC horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
XX CC treated include autoimmune diseases e.g. rheumatoid arthritis,
XX CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
XX CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
XX CC e.g. cerebral ischemia, angiogenesis, nervous system disorders,
XX CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
XX CC fungi and ocular disorders e.g. corneal infection. The polypeptides can
XX CC also be used to aid wound healing and epithelial cell proliferation,
XX CC to prevent skin aging due to sunburn, to maintain organs before
XX CC transplantation, for supporting cell culture of primary tissues, to
XX CC regenerate tissues and in chemotaxis. The polypeptides can also be used
XX CC as a food additive or preservative to increase or decrease storage
XX CC capabilities.
XX SQ Sequence 215 AA;
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Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HELSWAARRTGAHRHGCISIRSKWHICIKPEKARGKQKQLIFFPMSISSALAMVFMG 60
DB 1 HELSWAARRTGAHRHGCISIRSKWHICIKPEKARGKQKQLIFFPMSISSALAMVFMG 60
QY 61 AKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLVAINRTDTEYVLTANGLFGEKSYDFL 120
DB 61 AKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLVAINRTDTEYVLTANGLFGEKSYDFL 120
QY 121 TGFTDSCGKIFYQATIKQLDFVNDTEKSTTRVNSWVADTKAWKIIQTSLSHLEEPGIASS 180
DB 121 TGFTDSCGKIFYQATIKQLDFVNDTEKSTTRVNSWVADTKAWKIIQTSLSHLEEPGIASS 180
QY 181 SCYCKACLSQPLLVHSIPKCNPSVTPHGMWXPSSL 215
DB 181 SCYCKACLSQPLLVHSIPKCNPSVTPHGMWXPSSL 215
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XX AC AAO14914;
XX AC AAO14914;
XX DT 19-JUL-2002 (first entry)
XX XX Human serine protease inhibitor (serpin) HMCIS41.
XX KW Human, serine protease inhibitors; serpin; blood coagulation;
XX KW proteinase-activated physiological process; gene therapy;
XX KW antisense therapy; cancer; inflammation; neurological disease;
XX KW immune disease; HMCIS41.
XX OS Homo sapiens.
XX XX Key Location/Qualifiers

FT Misc-difference 211
FT /label= Unknown
FT /note= "Encoded by TGN"
XX PN WO200155390-A1.
XX PD 02-AUG-2001.
XX XX 26-JAN-2001; 2001WO-US02484.
XX PR 28-JAN-2000; 2000US-0178769.
XX PR 29-FEB-2000; 2000WO-US05082.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX NI Ni J, Ruben SM, Shi Y;
XX WPI; 2001-457730/49.
XX DR N-PSDB; AAL42746.
XX PT Isolated serine protease inhibitor polypeptide for treating, preventing
XX PT and/or prognosing cancers, inflammation, immune disorders and
XX PT neurological diseases and also for testing and detection e.g. diagnosis
XX PS Claim 12; Page 276-277; 288pp; English.
XX CC The invention comprises the amino acid and coding sequences of a group of
XX CC novel human serine protease inhibitors (serpins). Serpins are a
XX CC superfamily of single chain proteins that contain a conserved structure
XX CC of approximately 370-420 amino acids and generally range between 50 and
XX CC 100 kDa in molecular mass. The majority of serpins function as protease
XX CC inhibitors and so are involved in the regulation of several proteinase-
XX CC activated physiological processes (e.g. blood coagulation). The Serpin
XX CC DNA and amino acid sequences of the invention are useful in the treatment
XX CC (e.g. gene therapy, antisense therapy) and diagnosis of conditions such
XX CC as cancer, inflammation, neurological diseases and immune diseases. The
XX CC present amino acid sequence represents a human serpin protein of the
XX CC invention.
XX SQ Sequence 215 AA;
Query Match 99.8%; Score 1143; DB 22; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HELSWAARRTGAHRHGCISIRSKWHICIKPEKARGKQKQLIFFPMSISSALAMVFMG 60
DB 1 HELSWAARRTGAHRHGCISIRSKWHICIKPEKARGKQKQLIFFPMSISSALAMVFMG 60
QY 61 AKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLVAINRTDTEYVLTANGLFGEKSYDFL 120
DB 61 AKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLVAINRTDTEYVLTANGLFGEKSYDFL 120
QY 121 TGFTDSCGKIFYQATIKQLDFVNDTEKSTTRVNSWVADTKAWKIIQTSLSHLEEPGIASS 180
DB 121 TGFTDSCGKIFYQATIKQLDFVNDTEKSTTRVNSWVADTKAWKIIQTSLSHLEEPGIASS 180
QY 181 SCYCKACLSQPLLVHSIPKCNPSVTPHGMWXPSSL 215
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ID AAB08783 standard; Protein; 199 AA.
XX AC AAB08783;
XX XX 02-JAN-2001 (first entry)
XX DE Amino acid sequence of a human serpin polypeptide.
XX XX

Wed May 28 14:44:09 2003

QY 163 KIIOTSLHLEPGIASSCYCKACLSQPLLVHSPKCNPSVPTPHGMWXPSSL 215
Db 147 KIIOTSLHLEPGIASSCYCKACLSQPLLVHSPKCNPSVPTPHGMWXPSSL 199

RESULT 5
AAB08784
ID AAB08784 standard; Protein; 202 AA.
XX
AC AAB08784;
XX
DT 02-JAN-2001 (first entry)
XX
DE Amino acid sequence of a human serpin polypeptide.
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KW Human; serpin; serine protease inhibitor; autoimmune disease; neoplasm;
KW rheumatoid arthritis; hyperproliferative disorder; cerebral ischemia;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; epithelial cell proliferation;
KW skin aging; sunburn; wound healing; organ transplantation; chemotaxis;
KW food additive; food preservative.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 31 /note= "any L-amino acid which is encoded by NNN"
FT Misc-difference 32 /note= "any L-amino acid which is encoded by NNN"
FT Misc-difference 33 /note= "any L-amino acid which is encoded by NNN"
FT Misc-difference 198 /note= "any L-amino acid which is encoded by TGN"
XX
FN WO200052160-A1.
PN
PD 08-SEP-2000.
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PF 29-FEB-2000; 2000WO-US05082.
XX
PR 01-MAR-1999; 99US-0122276.
PR 12-MAR-1999; 99US-0124094.
PR 18-AUG-1999; 99US-0149452.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J;
XX
XX WPI; 2000-579284/54.
N-PSDB; AAA74935.
XX
PT Novel human serine protease inhibitor superfamily of proteins useful
PT for diagnosing, treating, preventing and/or prognosing disorders
PT related to the Serpin polypeptides
XX
PS Claim 12; Page 13-14; 215pp; English.
XX
CC The present sequence represents a human serpin polypeptide. Serpin is
CC a member of the serine protease inhibitor superfamily of polypeptides.
CC The serpin polynucleotides and polypeptides are used to prevent, treat
CC or ameliorate a medical conditions in e.g. humans, mice, rabbits, goats,
CC horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angioneurosis, nervous system disorders,
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. The polypeptides can
CC also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used

CC as a food additive or preservative to increase or decrease storage
XX capabilities.
SQ Sequence 202 AA;

Query Match 78.0%; Score 893; DB 21; Length 202;
Best Local Similarity 93.0%; Pred. No. 7.7e-91;
Matches 173; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 34 KARGKQLQLIFF-PMSSSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGF 89
Db 17 KLGNNNSNLFSSXXPMSSSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGF 76

QY 90 QSLLVAINRTDEYVLRNTANGLFGEKSYDPLTGTDSGKIFYOATIKQLDFVNDTEKSTT 149
Db 77 QSLLVAINRTDEYVLRNTANGLFGEKSYDPLTGTDSGKIFYOATIKQLDFVNDTEKSTT 136

QY 150 RVNSWADTKKANKIOTSLHLEPGIASSCYCKACLSQPLLVHSPKCNPSVPTPHGM 209
Db 137 RVNSWADTKKANKIOTSLHLEPGIASSCYCKACLSQPLLVHSPKCNPSVPTPHGM 196

QY 210 WXPSSL 215
Db 197 WXPSSL 202

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AC AAO14922;
XX
DT 19-JUL-2002 (first entry)
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DE Human serine protease inhibitor (serpin) 2.
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KW Human; serine protease inhibitors; serpin; blood coagulation;
KW proteinase-activated physiological process; gene therapy;
KW antiseptic therapy; cancer; inflammation; neurological disease;
KW immune disease.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT /note= "Encoded by NNN"
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FN WO200155390-A1.
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PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02484.
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PR 28-JAN-2000; 2000US-0178769.
PR 29-FEB-2000; 2000WO-US05082.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Ruben SM, Shi Y;
XX
XX WPI; 2001-457730/49.
DR N-PSDB; AAL42748.
XX

PT Isolated serine protease inhibitor polypeptide for treating, preventing
 PT and/or prognosing cancers, inflammation, immune disorders and
 PT neurological diseases and also for testing and detection e.g. diagnosis
 PT
 XX
 PS Claim 12, Page 15; 288pp; English.
 PS
 CC The invention comprises the amino acid and coding sequences of a group of
 CC novel human serine protease inhibitors (serpins). Serpins are a
 CC superfamily of single chain proteins that contain a conserved structure
 CC of approximately 370-420 amino acids and generally range between 50 and
 CC 100 kDa in molecular mass. The majority of serpins function as protease-
 CC inhibitors and so are involved in the regulation of several proteinase-
 CC activated physiological processes (e.g. blood coagulation). The Serpin
 CC DNA and amino acid sequences of the invention are useful in the treatment
 CC (e.g. gene therapy, antisense therapy) and diagnosis of conditions such
 CC as cancer, inflammation, neurological diseases and immune diseases. The
 CC present amino acid sequence represents a human serpin protein of the
 CC invention.

SQ Sequence 202 AA;

Query Match 78.0%; Score 893; DB 22; Length 202;
 Best Local Similarity 93.0%; Pred. No. 7.7e-91;
 Matches 173; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 34 KARGKQLKQIIFP----PMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGF 89
 DB 17 KKLGENNSNNLFFSPXXPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGF 76
 QY 90 QSLVAINRTDTEYVLRVTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTT 149
 DB 77 QSLVAINRTDTEYVLRVTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTT 136
 QY 150 RVNSWVADTKAWKIQTSLSHLEPGIASSSCYKACLSQPLLVHSPKCNSPVTPHGM 209
 DB 137 RVNSWVADTKAWKIQTSLSHLEPGIASSSCYKACLSQPLLVHSPKCNSPVTPHGM 196
 QY 210 WXPSSL 215
 DB 197 WXPSSL 202

RESULT 7
 AAB08777
 ID AAB08777 standard; Protein; 201 AA.

AAB08777;

02-JAN-2001 (first entry)

Amino acid sequence of a human serpin polypeptide.

Human; serpin; serine protease inhibitor; autoimmune disease; neoplasm;
 rheumatoid arthritis; hyperproliferative disorder; cerebral ischemia;
 cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 angiogenesis; nervous system disorder; Alzheimer's disease; infection;
 ocular disorder; corneal infection; epithelial cell proliferation;
 skin aging; sunburn; wound healing; organ transplantation; chemotaxis;
 food additive; food preservative.

Homo sapiens.

Key Location/Qualifiers
 Misc-difference 32 /note= "any L-amino acid"
 Misc-difference 33 /note= "any L-amino acid"
 Misc-difference 197 /note= "any L-amino acid"

WO200052160-A1.

PD 08-SEP-2000.
 XX
 PF 29-FEB-2000; 2000WO-US05082.
 XX
 PR 01-MAR-1999; 99US-0122276.
 PR 12-MAR-1999; 99US-0124094.
 PR 18-AUG-1999; 99US-0149452.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ni J;
 XX
 DR WPI; 2000-579284/54.
 XX

Novel human serine protease inhibitor superfamily of proteins useful
 for diagnosing, treating, preventing and/or prognosing disorders
 related to the serpin polypeptides

Claim 12; Page 12; 215pp; English.

The present sequence represents a human serpin polypeptide. Serpin is
 a member of the serine protease inhibitor superfamily of polypeptides.
 The serpin polynucleotides and polypeptides are used to prevent, treat
 or ameliorate a medical conditions in e.g. humans, mice, rabbits, goats,
 horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
 treated include autoimmune diseases e.g. rheumatoid arthritis,
 hyperproliferative disorders e.g. neoplasms of the breast or liver,
 cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 e.g. cerebral ischemia, angiogenesis, nervous system disorders,
 e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 fungi and ocular disorders e.g. corneal infection. The polypeptides can
 also be used to aid wound healing and epithelial cell proliferation,
 to prevent skin aging due to sunburn, to maintain organs before
 transplantation, for supporting cell culture of primary tissues, to
 regenerate tissues and in chemotaxis. The polypeptides can also be used
 as a food additive or preservative to increase or decrease storage
 capabilities.

SQ Sequence 201 AA;

Query Match 77.3%; Score 885.5; DB 21; Length 201;
 Best Local Similarity 93.0%; Pred. No. 5.2e-90;
 Matches 172; Conservative 2; Mismatches 8; Indels 3; Gaps 1;

QY 34 KARGKQLKQIIFP---MSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGF 90
 DB 17 KKLGENNSNNLFFSPXXPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGF 76

QY 91 SLLVAINRTDTEYVLRVTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTT 150
 DB 77 SLLVAINRTDTEYVLRVTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTT 136

QY 151 VNSWVADTKAWKIQTSLSHLEPGIASSSCYKACLSQPLLVHSPKCNSPVTPHGM 210
 DB 137 VNSWVADTKAWKIQTSLSHLEPGIASSSCYKACLSQPLLVHSPKCNSPVTPHGM 196

QY 211 XPPSL 215
 DB 197 XPPSL 201

RESULT 8

AAO14915
 ID AAO14915 standard; Protein; 201 AA.

AC AAO14915;

DT 19-JUL-2002 (first entry)

Human serine protease inhibitor (serpin) 3.

Human; serine protease inhibitors; serpin; blood coagulation;
 proteinase-activated physiological process; gene therapy;

antiseptic therapy; cancer; inflammation; neurological disease; immune disease.

Homo sapiens.

Key Location/Qualifiers
Misc-difference 32 /label= Unknown
Misc-difference 33 /label= Unknown
Misc-difference 197 /label= Unknown

WO200155390-A1.

02-AUG-2001.

26-JAN-2001; 2001WO-US02484.

28-JAN-2000; 2000US-0178769.

29-FEB-2000; 2000WO-US05082.

(HUMA-) HUMAN GENOME SCI INC.

Ni J, Ruben SM, Shi Y;

WPI; 2001-457730/49.

Isolated serine protease inhibitor polypeptide for treating, preventing and/or prognosing cancers, inflammation, immune disorders and neurological diseases and also for testing and detection e.g. diagnosis

Claim 12; Page 14; 288pp; English.

The invention comprises the amino acid and coding sequences of a group of novel human serine protease inhibitors (serpins). Serpins are a superfamily of single chain proteins that contain a conserved structure of approximately 370-420 amino acids and generally function as protease inhibitors and so are involved in the regulation of several proteinase-activated physiological processes (e.g. blood coagulation). The Serpin DNA and amino acid sequences of the invention are useful in the treatment (e.g. gene therapy, antisense therapy) and diagnosis of conditions such as cancer, inflammation, neurological diseases and immune diseases. The present amino acid sequence represents a human serpin protein of the invention.

Sequence 201 AA;

Query Match 77.3%; Score 885.5; DB 22; Length 201;
Best Local Similarity 93.0%; Pred. No. 5.2e-90;
Matches 172; Conservative 2; Mismatches 8; Indels 3; Gaps 1;

34 KARGKQLKLIFFP---MSISSALAMVFMGAKNTAAQMSQALCFSGKIGGEDGDIHRGQ 90

17 KLGNNNNLFFSPXMSISSALAMVFMGAKNTAAQMSQALCFSGKIGGEDGDIHRGQ 76

91 SLIVAINRTDTEVLTANGLFGEKSYDFLTGTDSCGKFPYQNTIKQLDFVNDTEKSTTR 150

77 SLIVAINRTDTEVLTANGLFGEKSYDFLTGTDSCGKFPYQNTIKQLDFVNDTEKSTTR 136

151 VNSWADTKAWKIQTSLSHLEPFGIASSSCYCKACLSQPLLVHSPKNSPVTPHGWM 210

137 VNSWADTKAWKIQTSLSHLEPFGIASSSCYCKACLSQPLLVHSPKNSPVTPHGWM 196

211 XPPSL 215

197 XPPSL 201

RESULT 9
ABG66743

ABG66743 standard; Protein; 170 AA.

ABG66743;

30-AUG-2002 (first entry)

Human novel polypeptide #78.

Human; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder; fungal infection.

Homo sapiens.

WO200244340-A2.

06-JUN-2002.

30-NOV-2001; 2001WO-US47004.

30-NOV-2000; 2000US-0028952.

(HYSE-) HYSEQ INC.

Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;
Yamazaki V, Ujwal ML, Drmanac RT;

WPI; 2002-508509/54.

N-PSDB; ABK94967.

Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing -

Claim 10; Page 654; 672pp; English.

The invention relates to human novel polynucleotides and associated polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthritis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia gravis, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences ABG66666-ABG66758 represent human novel polypeptides of the invention.

Sequence 170 AA;

Query Match 52.4%; Score 600; DB 23; Length 170;

Best Local Similarity 83.9%; Pred. No. 2.4e-58;

Matches 120; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 43 LIFFPMSISSALAMVFMGAKNTAAQMSQALCFSGKIGGEDGDIHRGQSLIVAINRTDTE 102

Db 27 LFFSPLSISALAWFMGAKGNTAAQMSQALCFSGKIGDGOIHRGFSLLVAINRTDTE 86
QY 103 YVLRRTANGLFGEKSYDFLTGFTDSCGKFOATIKQLDFVNDTEKSTTRVNSWADTKRAW 162
Db 87 YVLRRTANGLFGEKSYDFLTGFTDSCGKFOATIKQLDFVNDTEKSTTRVNSWADTKRGE 146
QY 163 KIIQTSLSHLEPFGIASSCYCK 185
Db 147 NILFEYFDNLSFVSSLQNCQ 169
RESULT 10
AAU02922
ID AAU02922 standard; Protein; 319 AA.
AC AAU02922;
XX 12-SEP-2001 (first entry)
DE Angiotensin converting enzyme (ACEV) splice variant protein #22.
XX
KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonarctoidic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.
XX
OS Homo sapiens.
XX
XX WO200136632-A2.
XX 25-MAY-2001.
XX 17-NOV-2000; 2000WO-IL00766.
XX 17-NOV-1999; 99IL-0132978.
XX 10-DEC-1999; 99IL-0133455.
XX (COMP-) COMPUGEN LTD.
XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX WPI; 2001-336004/35.
XX N-PSDB; AAS06022.
XX Novel alternative splicing variants e.g. variant of angiotensin
XX converting enzyme (ACEV), useful in identifying candidate compounds
XX capable of binding to the variant and to detect anti-variant antibodies
XX
XX Claim 4; Fig 22; 519pp; English.
XX The sequence represents an angiotensin converting enzyme splice variant
XX (ACEV) polypeptide. The polypeptides of the invention include variants of
XX granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
XX platelet-derived endothelial cell growth factor, cyclin-dependent kinase
XX inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
XX polypeptide receptor 2. The polypeptides and their associated nucleic
XX acids are useful for identification of variant sequences and detection of
XX the invention compounds capable of binding to the molecules. The sequences of
XX the invention can be used in the treatment and diagnosis of various
XX disorders including cardiovascular diseases such as arteriosclerosis,
XX myocardial infarction and coronary arterial thrombosis, renal diseases
XX such as diabetic nephropathy, muscular diseases such as hypertrophy,
XX immune disorders such as immune complex nephritis, multiple sclerosis,
XX cancer, sarcoidosis, nonarctoidic pulmonary granulomatous diseases such
XX as asbestosis and vascular pathologies involving an endothelial

CC abnormality such as deep vein thrombosis.
XX
SQ Sequence 319 AA;
Query Match 35.3%; Score 404.5; DB 22; Length 319;
Best Local Similarity 51.5%; Pred. No. 3.3e-36;
Matches 85; Conservative 29; Mismatches 36; Indels 15; Gaps 4;
QY 34 KARGKQLKQLIFF-PMSISSALAWFMGAKGNTAAQMSQALCFSGKIGDGOIHRGFSLL 92
Db 17 KTLGKDNSKNVFFSPMGMSALAWFMGAKGNTAAQMSQALCFSGKIGDGOIHRGFSLL 75
QY 93 LVAINRTDTEYVLRRTANGLFGEKSYDFLTGFTDSCGKFOATIKQLDFVNDTEKSTTRVN 152
Db 76 LTVNKTGTQYLLVAVNRLFGKSCDFLSSFRSCQFYQAEEMELDFISAVEKSRKHIN 135
QY 153 SWADTKTAWKIIQTSLSHLEPFGIASSCYCKACLSOPLLVHSI 197
Db 136 TWAEKTEG-----KIAELLSPGSVDP-----LTRLVLVNAV 167
RESULT 11
AAU02963
ID AAU02963 standard; Protein; 372 AA.
XX
AC AAU02963;
XX
DT 12-SEP-2001 (first entry)
XX
DE Angiotensin converting enzyme (ACEV) splice variant protein #63.
XX
KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonarctoidic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.
XX
OS Homo sapiens.
XX
XX WO200136632-A2.
XX 25-MAY-2001.
XX 17-NOV-2000; 2000WO-IL00766.
XX 17-NOV-1999; 99IL-0132978.
XX 10-DEC-1999; 99IL-0133455.
XX (COMP-) COMPUGEN LTD.
XX
XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX WPI; 2001-336004/35.
XX N-PSDB; AAS06063.
XX Novel alternative splicing variants e.g. variant of angiotensin
XX converting enzyme (ACEV), useful in identifying candidate compounds
XX capable of binding to the variant and to detect anti-variant antibodies
XX
XX Claim 4; Fig 63; 519pp; English.
XX The sequence represents an angiotensin converting enzyme splice variant
XX (ACEV) polypeptide. The polypeptides of the invention include variants of
XX granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
XX platelet-derived endothelial cell growth factor, cyclin-dependent kinase
XX inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
XX polypeptide receptor 2. The polypeptides and their associated nucleic
XX acids are useful for identification of variant sequences and detection of
XX the invention compounds capable of binding to the molecules. The sequences of
XX the invention can be used in the treatment and diagnosis of various
XX disorders including cardiovascular diseases such as arteriosclerosis,
XX myocardial infarction and coronary arterial thrombosis, renal diseases
XX such as diabetic nephropathy, muscular diseases such as hypertrophy,
XX immune disorders such as immune complex nephritis, multiple sclerosis,
XX cancer, sarcoidosis, nonarctoidic pulmonary granulomatous diseases such
XX as asbestosis and vascular pathologies involving an endothelial

acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonrheumatic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis.

[illegible]

RESULT 12
AAU02962
ID AAU02962 standard; Protein; 400 AA.
XX
XX AC
XX AC
XX DT 12-SEP-2001 (first entry)
XX
XX DE Angiotensin converting enzyme (ACEV) splice variant protein #62.
XX KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonrhegmatocytic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.

OS	Homo sapiens.
XX	
XX	WO200136632-A2.
XX	
XX	25-MAY-2001.
PD	
XX	
XX	17-NOV-2000; 200WO-IL00766.
PF	
XX	
XX	17-NOV-1999; 99IL-0132978.
PR	
PR	10-DEC-1999; 99IL-0133455.
XX	
XX	(COMP-) COMPUGEN LTD.
PA	
XX	
PI	Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX	
XX	WPI; 2001-336004/35.
DR	N-PSDB; AAS06062.
DR	
XX	
PT	Novel alternative splicing variants e.g. variant of angiotensin
PT	converting enzyme (ACEV), useful in identifying candidate compounds
PT	capable of binding to the variant and to detect anti-variant antibodies
PT	

XX
XX
XX
CC The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, nonrheumatoid pulmonary granulomatous diseases such
CC as asbestrosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis.

XX Sequence 400 AA;
XX

	Query Match	35.38;	Score 404.5;	DB 22;	Length 400;
	Best Local Similarity	51.59;	Pred. No. 4.6e-35;		
	Matches	85;	Conservative	Mismatches 36;	Indels 15; Gaps
Qy	34 KARGKQLKQLFF-PMSITSSALAMVFMCAKNTAAQNSQALCFKGIGGEDGDIHRGFOSL	92			
Dd	17 KTLGKDONSKNYFFSPMGSNCALAWYMGAKNTAAQWAILSFNKSQG-GGDIIHQGFOSL	75			
Qy	93 LVAINRTDTEVLVLTANGLFGEKSYDFLTGTDCSGKFYQATIKQLDFVNDEKSTTRVN	152			
Dd	76 LTVNKTTQTQLLRVANELLFGEKSCDFLSRFDSCQKPYQAEMELDPISAVEKSRKHIN	135			
Qy	153 SWVDADTKKWKI IOTSLSHLBEPGIASSCYCKACLSQLPLVHSI	197			
b	136 TWVAEFTG-----KTAFISPSGVDP-----LTRLVAVNAV	167			

RESULT 13	
AAU02974	AAU02974 standard; Protein; 204 AA.
ID	AAU02974 standard; Protein; 204 AA.
XX	
AC	AAU02974;
XX	
DT	12-SEP-2001 (first entry)
XX	
DE	Angiotensin converting enzyme (ACEV) splice variant protein #74.
XX	
XX	Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW	granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW	platelet-derived endothelial cell growth factor; cardiovascular disease;
KW	cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW	vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW	myocardial infarction; coronary arterial thrombosis; renal disease;
KW	diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW	multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW	noncardiotoxic pulmonary granulomatous disease; endothelial abnormality;
KW	vascular disorder; asbestosis.
XX	
OS	Homo sapiens.
XX	
PN	WC200136632-A2.
XX	
PD	25-MAY-2001.
XX	
XX	17-NOV-2000; 200WO-IL00766.
PF	
XX	
PR	17-NOV-1999; 99IL-0132978.
PR	10-DEC-1999; 99IL-013455.
XX	
XX	(COMP-) COMPUGEN LTD.
XX	

PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;
 DR WPI; 2001-336004/35.
 DR N-PSDB; AAS06074.
 XX
 PT Novel alternative splicing variants e.g. variant of angiotensin
 PT converting enzyme (ACEV), useful in identifying candidate compounds
 PT capable of binding to the variant and to detect anti-variant antibodies
 XX
 PS Claim 4; Fig 74; 519pp; English.
 XX
 CC The sequence represents an angiotensin converting enzyme splice variant
 CC (ACEV) polypeptide. The polypeptides of the invention include variants of
 CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
 CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
 CC inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
 CC polypeptide receptor 2. The polypeptides and their associated nucleic
 CC acids are useful for identification of variant sequences and detection of
 CC candidate compounds capable of binding to the molecules. The sequences of
 CC the invention can be used in the treatment and diagnosis of various
 CC disorders including cardiovascular diseases such as arteriosclerosis,
 CC myocardial infarction and coronary arterial thrombosis, renal diseases
 CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
 CC immune disorders such as immune complex nephritis, multiple sclerosis,
 CC cancer, sarcoidosis, nonaroidotic pulmonary granulomatous diseases such
 CC as asbestosis and vascular pathologies involving an endothelial
 CC abnormality such as deep vein thrombosis.

XX SQ Sequence 204 AA;
 Query Match 35.2%; Score 403.5; DB 22; Length 204;
 Best Local Similarity 51.5%; Pred. No. 2.2e-36;
 Matches 85; Conservative 29; Mismatches 36; Indels 15; Gaps 4;
 QY 34 KARGKQLQLIFF-PMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFSQL 92
 Db 17 KTLGKDNKSNVFFSPMSKSCALAMVYMGAKGNTAAQMAQILSFNKGSGG-GGDIHQGFQSL 75
 QY 93 LVAINRTDEYVLTANGLFGEKSYDPLTGFTDSCGKPYQATIKQLDFVNDTEKSTTRVN 152
 Db 76 LTVNKTQYLLRMANRLFGEKSCDFLSFRDSCQKPYQAEEMELDFISAVEKSRKHIN 135
 QY 153 SWADKTKAWKIQTSLSHLEPFIASSSCYCKACLSQPLLVHSI 197
 Db 136 TWAETEG-----KIAELSPGSVDP-----LTRLVLVNAV 167

RESULT 14
 AAB59176
 ID AAB59176 standard; Protein; 376 AA.

AC AAB59176;
 XX
 DT 22-MAR-2001 (first entry)
 XX
 DE Thrombin inhibitor protein.
 XX
 KW Thrombin inhibitor; human; thrombolytic; cardiant; cytostatic; nootropic;
 KW Parkinson's; tumour; deep venous thrombosis; pulmonary embolism;
 KW heart.
 XX
 OS Unidentified.
 XX
 PN US6156540-A.
 XX
 PD 05-DEC-2000.
 XX
 PF 22-DEC-1993; 93US-0171817.
 XX
 PR 22-DEC-1993; 93US-0171817.
 XX
 DR (HUMA-) HUMAN GENOME SCI INC.
 PA

XX Rosen CA, Fuldner RA, Cao L, Adams MD;
 XX WPI; 2001-060165/07.
 XX
 PT Novel polynucleotide encoding thrombin inhibitor polypeptide useful for
 PT diagnosis and treatment of diseases related to thrombosis -
 XX
 PS Claim 1; Fig 1; 19pp; English.
 XX
 CC The present invention relates to a thrombin inhibitor. This is useful
 CC for diagnosis and treatment of thrombosis, neurodegenerative diseases
 CC such as Alzheimer's disease and Parkinson's disease, tumor metastasis,
 CC to prevent proximal extension of deep venous thrombosis or the
 CC recurrence of pulmonary embolisms and also to treat risk patients who
 CC have congestive heart failure, acute myocardial infarction or
 CC cardiomyopathy to prevent the development of deep vein thrombosis or
 CC pulmonary embolism. The thrombin inhibitor is also useful for
 CC screening chemical compounds that either up or down regulate its
 CC activity.
 XX

SQ Sequence 376 AA;

Query Match 35.2%; Score 403.5; DB 22; Length 376;
 Best Local Similarity 51.5%; Pred. No. 5.5e-36;
 Matches 85; Conservative 29; Mismatches 36; Indels 15; Gaps 4;
 QY 34 KARGKQLQLIFF-PMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFSQL 92
 Db 17 KTLGKDNKSNVFFSPMSKSCALAMVYMGAKGNTAAQMAQILSFNKGSGG-GGDIHQGFQSL 75
 QY 93 LVAINRTDEYVLTANGLFGEKSYDPLTGFTDSCGKPYQATIKQLDFVNDTEKSTTRVN 152
 Db 76 LTVNKTQYLLRMANRLFGEKSCDFLSFRDSCQKPYQAEEMELDFISAVEKSRKHIN 135
 QY 153 SWADKTKAWKIQTSLSHLEPFIASSSCYCKACLSQPLLVHSI 197
 Db 136 TWAETEG-----KIAELSPGSVDP-----LTRLVLVNAV 167

RESULT 15
 AAB11125
 ID AAB11125 standard; Protein; 376 AA.

AC AAB11125;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Human thrombin inhibitor protein.
 XX
 KW Thrombin inhibitor; human; thrombolytic; cardiant; cytostatic; nootropic;
 KW neuroprotective; antiparkinsonian; gene therapy; treatment; carcinoma;
 KW cell hypercoagulation; deep venous thrombosis; pulmonary embolism;
 KW cerebral embolism; thrombic disease; tumor metastases; clot accretion;
 KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease.
 XX
 OS Homo sapiens.
 XX
 PN US6133422-A.
 XX
 PD 17-OCT-2000.
 XX
 PF 30-NOV-1998; 98US-0200965.
 XX
 PR 22-DEC-1993; 93US-0171817.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Fuldner RA, Rosen CA, Cao L, Adams MD;
 DR WPI; 2001-006150/01.
 DR N-PSDB; AAC65737.

Wed May 28 14:44:09 2003

PT New thrombin inhibiting proteins for treating or preventing
PT thrombosis-related diseases, e.g. embolism, tumor metastases,
PT carcinoma, neurodegenerative diseases, e.g. Alzheimer's or Parkinson's
PT disease
XX
XX Claim 2; Column 17-20; 19pp; English.
XX
XX This invention describes a novel human thrombin inhibitor which has
CC thrombolytic, cardiant, cytostatic, neurotropic, neuroprotective and
CC antiparkinsonian activity and can be used for gene therapy. The thrombin
CC inhibitor may be used therapeutically or diagnostically to treat or
CC prevent diseases related to thrombosis characterized by hypercoagulation
CC of cells. The protein may also be used to prevent extension of deep
CC venous thrombosis of the recurrence of pulmonary embolisms and
CC recurrence of cerebral or other systemic embolisms, to treat high risk
CC patients, e.g. those who have congestive heart failure, acute myocardial
CC infarction or cardiomyopathy to prevent the development of deep vein
CC thrombosis or pulmonary embolism, and as long term therapy for occasional
CC patient who has recurrent thrombosis or embolism while on the drug
CC warfarin. The protein may also be used for treating thrombotic disease,
CC tumor metastases, carcinoma of the brain, liver, lung, bone and
CC neoplastic plasma cell carcinoma, and neurodegenerative diseases (e.g.
CC Alzheimer's or Parkinson's disease). It can also be used against
CC clot-bound thrombin, which produces clot accretion, for screening
CC chemical compounds that either up or down regulate its activity, and for
CC producing antibodies. The thrombin inhibitor can be used as
CC pharmaceutical to mammals, such as humans, mice, rats, hamster, dogs,
CC rabbits and cats. The cDNA sequences of the thrombin inhibitor may be
CC used as diagnostic probe, for chromosome identification.
XX
SQ Sequence 376 AA;

Query Match 35.2%; Score 403.5; DB 22; Length 376;
Best Local Similarity 51.5%; Pred. No. 5.5e-36;
Matches 85; Conservative 29; Mismatches 36; Indels 15; Gaps 4;
QY 34 KARGQLKQLIFF-PMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGQSL 92
Db 17 KTLGKDNKSNVFFSPMSMSALAMVFMGAKGNTAAQMAQLISFNKSGG-GGDIHGGQSL 75
QY 93 LVAINRTDTEYVLRVLTANGLFGEKSYDFLTGFTDSCGKPYQATIKOLDVFNDEKSTTRVN 152
Db 76 LTVNKVTGTQYLLRWANRIFGEKSCDFLSSFRDSCQKPYQAEEMELDFISAVEKSRKHIN 135
QY 153 SWVADKTKAWKIIQISLHLEPGIASSSCYCKACLSQELLVHSI 197
Db 136 TWVAEXTG-----KIAELLSPGSVDP-----LTRLVLVNAV 167

Search completed: May 20, 2003, 10:24:01
Time : 78 secs


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Db 17 KTLGKNSKNVFPSPMSALAMVFMGAKNTAAQMAQILSPFNKSGG-GGDIHQGFQSL 75
; Sequence 2, Application US/08385500
; Patent No. 5712117
; GENERAL INFORMATION:
; APPLICANT: Spracher, Cindy A.
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,500
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-385-500-2

Query Match 34.3%; Score 392.5; DB 1; Length 374;
Best Local Similarity 52.9%; Pred. No. 9e-37;
Matches 83; Conservative 23; Mismatches 34; Indels 17; Gaps 3;

QY 41 KQLIFFPMSISSALAMVFMGAKNTAAQMSQALCFSGKIGGEDGDIHRGFQSLVAINRTD 100
Db 26 RNVEFPMSISSALAMVFMGAKNTAAQMSQALCLYK----DGDIIHRGFQSLSEVNRTG 81
QY 101 TEVVLRTANGLFGEKSYDFLTGTDSCKFYQATIKQLDFVNDTEKSTTRVNSWADKTK 160
Db 82 TQYLLRTANLFGKTCDFLPDFKEYCQFYQAELELSFAEDTEBCRKHINDWVAEKTE 141
QY 161 AWKIIQTSLSHLEPFGIASSCCYKACLSQPLLVHSI 197
Db 142 G-----KISEVLDAAGTVDP-----LTKLVLVNAI 165

RESULT 4
US-08-846-784-2
; Sequence 2, Application US/08846784
; Patent No. 5747645
; GENERAL INFORMATION:
; APPLICANT: Spracher, Cindy A.
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

Db 17 KTLGKNSKNVFPSPMSALAMVFMGAKNTAAQMAQILSPFNKSGG-GGDIHQGFQSL 75
; Sequence 2, Application US/08464148
; Patent No. 5710026
; GENERAL INFORMATION:
; APPLICANT: Spracher, Cindy A.
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,148
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/385,500
; FILING DATE: 08-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-464-148-2

Query Match 34.3%; Score 392.5; DB 1; Length 374;
Best Local Similarity 52.9%; Pred. No. 9e-37;
Matches 83; Conservative 23; Mismatches 34; Indels 17; Gaps 3;

QY 41 KQLIFFPMSISSALAMVFMGAKNTAAQMSQALCFSGKIGGEDGDIHRGFQSLVAINRTD 100
Db 26 RNVEFPMSISSALAMVFMGAKNTAAQMSQALCLYK----DGDIIHRGFQSLSEVNRTG 81
QY 101 TEVVLRTANGLFGEKSYDFLTGTDSCKFYQATIKQLDFVNDTEKSTTRVNSWADKTK 160
Db 82 TQYLLRTANLFGKTCDFLPDFKEYCQFYQAELELSFAEDTEBCRKHINDWVAEKTE 141
QY 161 AWKIIQTSLSHLEPFGIASSCCYKACLSQPLLVHSI 197
Db 142 G-----KISEVLDAAGTVDP-----LTKLVLVNAI 165

RESULT 3
US-08-385-500-2
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,784
FILING DATE: 30-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/385,500
FILING DATE: 08-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-21
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-784-2

Query Match 34.3%; Score 392.5; DB 1; Length 374;
Best Local Similarity 52.9%; Pred. No. 9e-37;
Matches 83; Conservative 23; Mismatches 34; Indels 17; Gaps 3;
QY 41 KOLIFFPMSISSALAMVPMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLLVAINRTD 100
DB 26 RNVFSPMSISSALAMVPMGAKGNTAAQMSQALCLYK---DGDTHRGFQSLSEVNRGTG 81
QY 101 TEYVLTANGLFGEKSYDFLTGFTDSCGKEYQATIKOLDPVDNTEKSTTRVNSWVADTK 160
DB 82 TOYLLRTANRLFGKTCDFLPDFKEYCKFKYQAELELSFADTEECRKHNDWVAEKTE 141
QY 161 AWKIQTSLSHLEPGFIASSCYCKACLSQPLLVHSI 197
DB 142 G-----KISEVLDAAGTVDP-----LTKLVLVNAI 165

RESULT 5
US-08-464-148-4
Sequence 4, Application US/08464148
Patent No. 5710026
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,148
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/385,500
FILING DATE: 08-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 13952-21
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-148-4

Query Match 27.9%; Score 320; DB 1; Length 376;
Best Local Similarity 46.3%; Pred. No. 2e-28;
Matches 68; Conservative 28; Mismatches 45; Indels 6; Gaps 2;
QY 47 PMSISSALAMVPMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLLVAINRTDTEYVLR 106
DB 32 PVSISSALAMVLLGAKGNTATQMAQALSLN---TEEDIHRAFQSLLTENVKAGTQYLLR 87
QY 107 TANGLFGEKSYDFLTGFTDSCGKEYQATIKOLDPVDNTEKSTTRVNSWVADTK--KAWKI 164
DB 88 TANRLFGKTCQFLSTFKESCCLQFYHAELELSFADTEECRKHNDWVAEKTEEL 147
QY 165 IQTSLSHLEPGFIASSCYCKACLSQP 191
DB 148 LPGSSIDAETRLVLVNAIYFKGKWNKP 174

RESULT 6
US-08-385-500-4
Sequence 4, Application US/08385500
Patent No. 5712117
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,500
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-21
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-385-500-4

Query Match 27.9%; Score 320; DB 1; Length 376;
Best Local Similarity 46.3%; Pred. No. 2e-28;
Matches 68; Conservative 28; Mismatches 45; Indels 6; Gaps 2;

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QY 47 PMSISSALAWFMGKGNTRAAQMSQALCFKSGKIGGDIHRGFQSLVAINRTDTEYVLR 106
Db 32 PVSISALAWVLLGKAGNTATQMAQSLN-----TEEDIHRAFOQLLTVNVNKAQTQYLLR 87
QY 107 TANGLFGEKSYDFLTGFTDSCGKYQATIKQLDFVNDTEKSTTRVNSWVADKT--KAWKI 164
Db 88 TANLFGKTEQTLSTFKESCLQFYHAELKELSFIRAAEESRKHINTVWSKKTGKIEEL 147
QY 165 IOTSLHLEEPGIASSSCYCKACLSQP 191
Db 148 LPGSSIDAETRLVLVNAIFYKGNWEP 174

RESULT 7
US-08-846-784-4
; Sequence 4, Application US/08846784
; Patent No. 5747645
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,784
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/385,500
; FILING DATE: 08-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-784-4

Query Match 27.9%; Score 320; DB 1; Length 376;
Best Local Similarity 46.3%; Pred. No. 2e-28;
Matches 68; Conservative 28; Mismatches 45; Indels 6; Gaps 2;

QY 47 PMSISSALAWFMGKGNTRAAQMSQALCFKSGKIGGDIHRGFQSLVAINRTDTEYVLR 106
Db 32 PVSISALAWVLLGKAGNTATQMAQSLN-----TEEDIHRAFOQLLTVNVNKAQTQYLLR 87
QY 107 TANGLFGEKSYDFLTGFTDSCGKYQATIKQLDFVNDTEKSTTRVNSWVADKT--KAWKI 164
Db 88 TANLFGKTEQTLSTFKESCLQFYHAELKELSFIRAAEESRKHINTVWSKKTGKIEEL 147
QY 165 IOTSLHLEEPGIASSSCYCKACLSQP 191
Db 148 LPGSSIDAETRLVLVNAIFYKGNWEP 174
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RESULT 8
US-08-568-147B-2
; Sequence 2, Application US/08568147B
; Patent No. 5783422
; GENERAL INFORMATION:
; APPLICANT: Suminami, Yoshinori
; APPLICANT: Kato, Hiroshi
; APPLICANT: Sekiguchi, Kiyoshi
; APPLICANT: Takeda, Katsumichi
; TITLE OF INVENTION: DNA FRAGMENT CODING FOR SQUAMOUS CELL
; TITLE OF INVENTION: CARCINOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,147B
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 800,952
; FILING DATE: 02-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8425
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-568-147B-2

Query Match 23.2%; Score 266; DB 1; Length 390;
Best Local Similarity 37.9%; Pred. No. 3.4e-22;
Matches 53; Conservative 28; Mismatches 47; Indels 12; Gaps 1;

QY 32 FEKARGKQLQIIFPMSISSALAWFMGKGNTRAAQMSQALCFKSGKIG----- 79
Db 16 FOQFKSKENNIFYSPISITSLGCVLLGAKDNTAQQIKVLHFDQVTNTTGAATVHV 75
QY 80 GEDGDIHRGFQSLVAINRTDTEYVLTANGLFGEKSYDFLTGFTDSCGKYQATIKQLD 139
Db 76 DRSGNVHVFQKLLTFEKNKSTDAYELKIANKLFGKTYLFLQEYLDIAKKFYQTSVESVD 135
QY 140 FVNDTEKSTTRVNSWVADKT 159
Db 136 FANAPESRRKKNWSVESQT 155

RESULT 9
US-09-266-910-3
; Sequence 3, Application US/09266910
; Patent No. 6344362
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Use of a recombinant protein as receptor of a
; TITLE OF INVENTION: hepatitis virus
; NUMBER OF SEQUENCES: 8
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,910
FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-266-910-3

Query Match 23.0%; Score 263; DB 4; Length 390;
Best Local Similarity 37.9%; Pred. No. 7.6e-22;
Matches 53; Conservative 27; Mismatches 48; Indels 12; Gaps 1;

QY 32 FEKARGKQLKQLIFFPMSTISSALAMVFMGAKGNTAAQMSQALCFESKIG----- 79
DB 16 FQPRKSKENNIFYSPIISALGVLLGAKDNTAQIKKVLHFDQVTTNTGKAATYHV 75
QY 80 GEDGDIHRGFSQSLVAINRTDTEYVLTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLD 139
DB 76 DRSGNVHHQFQKLLTFEKNKSTDAVELKIANKLFGEKTYLFLOEYLDAIKKFYQTSVESVD 135
QY 140 FVNDTEKSTTRVNSWADKT 159
DB 136 FANAPESPCKINSWVESQT 155

RESULT 10
US-09-266-910-4
Sequence 4, Application US/09266910
Patent No. 6344362
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Use of a recombinant protein as receptor of a
NUMBER OF SEQUENCES: 8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,910
FILING DATE:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-266-910-4

Query Match 23.0%; Score 263; DB 4; Length 390;
Best Local Similarity 37.9%; Pred. No. 7.6e-22;
Matches 53; Conservative 27; Mismatches 48; Indels 12; Gaps 1;

QY 32 FEKARGKQLKQLIFFPMSTISSALAMVFMGAKGNTAAQMSQALCFESKIG----- 79
DB 16 FQPRKSKENNIFYSPIISALGVLLGAKDNTAQIKKVLHFDQVTTNTGKAATYHV 75
QY 80 GEDGDIHRGFSQSLVAINRTDTEYVLTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLD 139
DB 76 DRSGNVHHQFQKLLTFEKNKSTDAVELKIANKLFGEKTYLFLOEYLDAIKKFYQTSVESVD 135
QY 140 FVNDTEKSTTRVNSWADKT 159
DB 136 FANAPESPCKINSWVESQT 155

DB 76 DRSGNVHHQFQKLLTFEKNKSTDAVELKIANKLFGEKTYLFLOEYLDAIKKFYQTSVESVD 135
QY 140 FVNDTEKSTTRVNSWADKT 159
DB 136 FANAPESPCKINSWVESQT 155

RESULT 11
US-08-121-714-8
Sequence 8, Application US/08121714
Patent No. 5470970
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,714
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/072001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 375
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-121-714-8

Query Match 22.4%; Score 257; DB 1; Length 375;
Best Local Similarity 46.5%; Pred. No. 3.5e-21;
Matches 53; Conservative 19; Mismatches 38; Indels 4; Gaps 1;

QY 47 PMSISSALAMVFMGAKGNTAAQMSQALCFESKIGGEDIHRGFSQSLVAINRTDTEYVLR 106
DB 32 PLSISSALAMIFLGTRGNTAAQVSKALYFDTV-----EDIHSRFQSLNADINKPGAPYILK 87
QY 107 TANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWADKT 160
DB 88 LANRLYGEKTYNFLADFLASTQKMYGAEIASVDFQQAPEADARKEINWVKGOTE 141

RESULT 12
US-08-477-108A-8
Sequence 8, Application US/08477108A
Patent No. 5801001
GENERAL INFORMATION:

APPLICANT: Sager, Ruth
APPLICANT: Zou, Zhiqiang
APPLICANT: Anisowicz, Anthony
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
TUMOR SUPPRESSING ACTIVITY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,108A
FILING DATE: June 7, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/121,714
FILING DATE: 09/01/93
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06570/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 375
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-477-108A-8
Query Match 22.4%; Score 257; DB 1; Length 375;
Best Local Similarity 46.5%; Pred. No. 3.5e-21;
Matches 53; Conservative 19; Mismatches 38; Indels 4; Gaps 1;
QY 47 PMSISSALAMVFMGAKGNATQAQMSQALCFSGKIGGEDGDIHRGFSQSLVAINRTDTEYVLR 106
Db 32 PLSISSALAMIFLGRGNTAAQVSKALYFDTV----EDIHSRFSQSLNADINKPGAPYILK 87
QY 107 TANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADTK 160
Db 88 LANRLYGEKTYNFLADFLASTQKMYGAELASVDFOQAPEDARKEINWVKGQTE 141
RESULT 13
US-08-477-112-8
Sequence 8, Application US/08477112
Patent No. 5905023
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
TUMOR SUPPRESSING ACTIVITY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,112
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/121,714
FILING DATE: 09/01/93
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06570/002003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 375
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-477-112-8
Query Match 22.4%; Score 257; DB 2; Length 375;
Best Local Similarity 46.5%; Pred. No. 3.5e-21;
Matches 53; Conservative 19; Mismatches 38; Indels 4; Gaps 1;
QY 47 PMSISSALAMVFMGAKGNATQAQMSQALCFSGKIGGEDGDIHRGFSQSLVAINRTDTEYVLR 106
Db 32 PLSISSALAMIFLGRGNTAAQVSKALYFDTV----EDIHSRFSQSLNADINKPGAPYILK 87
QY 107 TANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADTK 160
Db 88 LANRLYGEKTYNFLADFLASTQKMYGAELASVDFOQAPEDARKEINWVKGQTE 141
RESULT 14
PCT-US93-08322-8
Sequence 8, Application PC/TUS9308322
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08322
FILING DATE:
CLASSIFICATION:

RESULT 15
 US-07-768-286B-6
 ; Sequence 6, Application US/07768286B
 ; Patent No. 5444153
 ; GENERAL INFORMATION:
 ; APPLICANT: GOSS, Neil H.
 ; APPLICANT: RICHARDSON, Michael A.
 ; TITLE OF INVENTION: VARIANTS OF PAI-2
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07768, 286B
 ; FILING DATE: 19911011
 ; CLASSIFICATION: 514
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/AU90/00603
 ; FILING DATE: 20-DEC-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 16786/157 CHAC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)836-9300
 ; TELEFAX: (703)683-4109
 ; TELEX: 899149
 ; INFORMATION FOR SEQ ID NO: 6:

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OM protein - protein search, using sw model

Run on: May 20, 2003, 10:26:02 ; Search time 56 Seconds
(without alignments)
380.752 Million cell updates/sec

Title: US-09-912-628-7
Perfect score: 1145
Sequence: 1 HELR5WAAARRTGARRHGCS.....SIPKCN5PVTPHGMWXPSSL 215
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues
1 number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1143	99.8	215	9	US-10-116-166-5
3	896	78.3	199	9	US-09-912-628-15
4	896	78.3	199	9	US-10-116-166-13
5	893	78.0	202	9	US-09-912-628-17
6	893	78.0	202	9	US-10-116-166-15
7	885.5	77.3	201	9	US-09-912-628-8
8	885.5	77.3	201	9	US-10-116-166-6
9	403.5	35.2	439	10	US-09-925-300-1440
10	392.5	34.3	374	9	US-09-974-298-95
11	278	24.3	330	1	US-08-731-566-2
12	240	21.0	437	10	US-09-925-301-1200
13	229	20.0	41	9	US-09-912-628-13
14	229	20.0	41	9	US-10-116-166-11
15	224	19.6	391	10	US-09-735-705-110
16	224	19.6	391	10	US-09-850-716A-110
17	224	19.6	391	10	US-09-897-778-110
18	223.5	19.5	415	10	US-09-902-684-4
19	222	19.4	42	9	US-09-912-628-11

20	222	19.4	42	9	US-10-116-166-9	Sequence 9, Appli
21	219.5	19.2	400	10	US-09-735-705-112	Sequence 112, App
22	219.5	19.2	400	10	US-09-850-716A-112	Sequence 112, App
23	219.5	19.2	400	10	US-09-897-778-112	Sequence 112, App
24	200	17.5	39	9	US-09-912-628-10	Sequence 10, Appli
25	200	17.5	39	9	US-10-116-166-8	Sequence 8, Appli
26	198	17.3	617	9	US-09-895-814-947	Sequence 947, App
27	198	17.3	617	9	US-09-895-814-947	Sequence 947, App
28	197	17.2	38	9	US-09-912-628-12	Sequence 12, Appli
29	197	17.2	38	9	US-10-116-166-10	Sequence 10, Appli
30	196	17.1	379	9	US-10-012-896-946	Sequence 946, App
31	196	17.1	379	9	US-09-895-814-946	Sequence 946, App
32	196	17.1	413	9	US-10-222-857-4	Sequence 4, Appli
33	186.5	16.3	418	9	US-10-135-629-2	Sequence 2, Appli
34	185.5	16.2	418	9	US-10-135-629-1	Sequence 1, Appli
35	175	15.3	380	9	US-10-091-442-34	Sequence 34, Appli
36	175	15.3	380	10	US-09-140-719-34	Sequence 34, Appli
37	174	15.2	315	1	US-08-731-566-4	Sequence 4, Appli
38	174	15.2	363	10	US-09-755-665-58	Sequence 58, Appli
39	173.5	15.2	377	9	US-10-165-605A-27	Sequence 27, Appli
40	173.5	15.2	377	10	US-09-910-430-27	Sequence 27, Appli
41	170	14.8	418	9	US-09-924-340-92	Sequence 92, Appli
42	170	14.8	418	9	US-09-952-600A-92	Sequence 92, Appli
43	170	14.8	418	9	US-10-000-489-92	Sequence 92, Appli
44	169	14.8	394	9	US-09-993-180-6	Sequence 6, Appli
45	169	14.8	394	9	US-10-025-514-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-912-628-7
; Sequence 7, Application US/09912628
; Patent No. US20020160491A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT001P2
; CURRENT APPLICATION NUMBER: US/09/912,628
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: PCT/US01/02484
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,769
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US00/05082
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (211)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-912-628-7
Query Match 99.8%; Score 1143; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 5.7e-114;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HELR5WAAARRTGARRHGCSIRSKWHICIKPEKARGKOLKQLIFPMSISSALAMVFMG 60
Db 1 HELR5WAAARRTGARRHGCSIRSKWHICIKPEKARGKOLKQLIFPMSISSALAMVFMG 60
QY 61 AKGNTAAQMSQALCFSGKIGEDGDIIHRGFQSLIVAINRTDTEYVLTANGLFGEKSYDFL 120
Db 61 AKGNTAAQMSQALCFSGKIGEDGDIIHRGFQSLIVAINRTDTEYVLTANGLFGEKSYDFL 120
QY 121 TGFTDCSGFYQNTIKQLDPVNDTEKSTRVNSWADKTKAWKIOTSLSHLEEGIAS 180

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Db 121 TGFTDSCGKGYQATIKQLDFVNDTEKSTTRVNSWVADTKAWKIQTSLSHLEPGLASS 180
Qy 181 SCYKACLSQPLLVHSIPKCNSPVTPHGMWXPPL 215
Db 181 SCYKACLSQPLLVHSIPKCNSPVTPHGMWXPPL 215

RESULT 2
US-10-116-166-5
; Sequence 5, Application US/10116166
; Publication No. US20030040097A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT001P1
; CURRENT APPLICATION NUMBER: US/10/116,166
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/641,721
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: PCT/US00/05092
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/122,276
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 60/124,094
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/149,452
; PRIOR FILING DATE: 1999-08-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (211)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-116-166-5
Query Match 99.8%; Score 1143; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 5,7e-114;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HELSWAARTGAHRHCCSIRSKWHICIKPEKARGKOLKQLIFFPMSISSALAMVFMG 60
Db 1 HELSWAARTGAHRHCCSIRSKWHICIKPEKARGKOLKQLIFFPMSISSALAMVFMG 60
Qy 61 AKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLLVAINRTDTEYVLRVLTANGLFGEKSYDFL 120
Db 61 AKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLLVAINRTDTEYVLRVLTANGLFGEKSYDFL 120
Qy 121 TGFTDSCGKGYQATIKQLDFVNDTEKSTTRVNSWVADTKAWKIQTSLSHLEPGLASS 180
Db 121 TGFTDSCGKGYQATIKQLDFVNDTEKSTTRVNSWVADTKAWKIQTSLSHLEPGLASS 180
Qy 181 SCYKACLSQPLLVHSIPKCNSPVTPHGMWXPPL 215
Db 181 SCYKACLSQPLLVHSIPKCNSPVTPHGMWXPPL 215

RESULT 3
US-09-912-628-15
; Sequence 15, Application US/09912628
; Patent No. US20020160491A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT001P2
; CURRENT APPLICATION NUMBER: US/09/912,628
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: PCT/US01/02484
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,769
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; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US00/05082
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (195)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-912-628-15
Query Match 78.3%; Score 896; DB 9; Length 199;
Best Local Similarity 98.8%; Pred. No. 1,2e-87;
Matches 171; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 43 LIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLLVAINRTDTE 102
Db 27 LFFSPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLLVAINRTDTE 86
Qy 103 YVLRVLTANGLFGEKSYDFLTGFTDSCGKGYQATIKQLDFVNDTEKSTTRVNSWVADTKAW 162
Db 87 YVLRVLTANGLFGEKSYDFLTGFTDSCGKGYQATIKQLDFVNDTEKSTTRVNSWVADTKAW 146
Qy 163 KIQTSLSHLEPGLASSCYCKACLSQPLLVHSIPKCNSPVTPHGMWXPPL 215
Db 147 KIQTSLSHLEPGLASSCYCKACLSQPLLVHSIPKCNSPVTPHGMWXPPL 199

RESULT 4
US-10-116-166-13
; Sequence 13, Application US/10116166
; Publication No. US20030040097A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT001P1
; CURRENT APPLICATION NUMBER: US/10/116,166
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/641,721
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: PCT/US00/05092
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/122,276
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 60/124,094
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/149,452
; PRIOR FILING DATE: 1999-08-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (195)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-116-166-13
Query Match 78.3%; Score 896; DB 9; Length 199;
Best Local Similarity 98.8%; Pred. No. 1,2e-87;
Matches 171; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 43 LIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLLVAINRTDTE 102
Db 27 LFFSPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLLVAINRTDTE 86
Qy 103 YVLRVLTANGLFGEKSYDFLTGFTDSCGKGYQATIKQLDFVNDTEKSTTRVNSWVADTKAW 162
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Db 87 YVLRNGLFGEKSYDFTGTCGKFYQATIKQLDFVNDTEKSTTRVNSWADKTAW 146
QY 163 KIIQTSLSHLEPFGIASSCYCKACLSQPLLHSHIPKCNKSPVTPHGMWPPSL 215
Db 147 KIIQTSLSHLEPFGIASSCYCKACLSQPLLHSHIPKCNKSPVTPHGMWPPSL 199

RESULT 5
US-09-912-628-17
; Sequence 17, Application US/09912628
; Patent No. US20020160491A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT001P2
; CURRENT APPLICATION NUMBER: US/09/912,628
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: PCT/US01/02484
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,769
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US00/05082
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (31)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (33)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-912-628-17

Query Match 78.0%; Score 893; DB 9; Length 202;
Best Local Similarity 93.0%; Pred. No. 2.5e-87;
Matches 173; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 34 KARGKQLKLIFF---PMSISSALAMVFMGAKGNTAAQMSQALCFKSKIGGEDGDIHRGF 89
Db 17 KLGGENNSNNLFFSXXXPMSSISSALAMVFMGAKGNTAAQMSQALCFKSKIGGEDGDIHRGF 76

QY 90 QSLVAINRDTTEYVLRNGLFGEKSYDFTGTCGKFYQATIKQLDFVNDTEKSTT 149
Db 77 QSLVAINRDTTEYVLRNGLFGEKSYDFTGTCGKFYQATIKQLDFVNDTEKSTT 136

QY 150 RVNSWADKTKAWKIIQTSLSHLEPFGIASSCYCKACLSQPLLHSHIPKCNKSPVTPHGM 209
Db 137 RVNSWADKTKAWKIIQTSLSHLEPFGIASSCYCKACLSQPLLHSHIPKCNKSPVTPHGM 196

QY 210 WXPSSL 215
Db 197 WXPSSL 202

RESULT 6
US-10-116-166-15
; Sequence 15, Application US/10116166
; Publication No. US20030040097A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies

; FILE REFERENCE: PT001P1
; CURRENT APPLICATION NUMBER: US/10/116,166
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/641,721
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: PCT/US00/05092
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/122,276
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 60/124,094
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/149,452
; PRIOR FILING DATE: 1999-08-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (31)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (33)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-10-116-166-15

Query Match 78.0%; Score 893; DB 9; Length 202;
Best Local Similarity 93.0%; Pred. No. 2.5e-87;
Matches 173; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

QY 34 KARGKQLKLIFF---PMSISSALAMVFMGAKGNTAAQMSQALCFKSKIGGEDGDIHRGF 89
Db 17 KLGGENNSNNLFFSXXXPMSSISSALAMVFMGAKGNTAAQMSQALCFKSKIGGEDGDIHRGF 76

QY 90 QSLVAINRDTTEYVLRNGLFGEKSYDFTGTCGKFYQATIKQLDFVNDTEKSTT 149
Db 77 QSLVAINRDTTEYVLRNGLFGEKSYDFTGTCGKFYQATIKQLDFVNDTEKSTT 136

QY 150 RVNSWADKTKAWKIIQTSLSHLEPFGIASSCYCKACLSQPLLHSHIPKCNKSPVTPHGM 209
Db 137 RVNSWADKTKAWKIIQTSLSHLEPFGIASSCYCKACLSQPLLHSHIPKCNKSPVTPHGM 196

QY 210 WXPSSL 215
Db 197 WXPSSL 202

RESULT 7
US-09-912-628-8
; Sequence 8, Application US/09912628
; Patent No. US20020160491A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT001P2
; CURRENT APPLICATION NUMBER: US/09/912,628
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: PCT/US01/02484
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,769
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US00/05082
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 8
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (33)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (197)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-912-628-8

Query Match 77.3%; Score 885.5; DB 9; Length 201;
Best Local Similarity 93.0%; Pred. No. 1.6e-86;
Matches 172; Conservative 2; Mismatches 8; Indels 3; Gaps 1;

34 KARGKQLKLIFFP---MSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQ 90
17 KKLGENNNLFFSPXXMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQ 76

QY 91 SLVAINRTDTEYVLTANGLFGEKSYDFTGTDSCGKGYQATIKQLDFVNDTEKSTTR 150
DB 77 SLVAINRTDTEYVLTANGLFGEKSYDFTGTDSCGKGYQATIKQLDFVNDTEKSTTR 136

QY 151 VNSWADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSIPKCNSPVTPHGMW 210
DB 137 VNSWADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSIPKCNSPVTPHGMW 196

QY 211 XPPSL 215
DB 197 XPPSL 201

RESULT 8
US-10-116-166-6
; Sequence 6, Application US/10116166
; Publication No. US20030040097A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT001F1
; CURRENT APPLICATION NUMBER: US/10/116,166
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/641,721
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: PCT/US00/05092
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/122,276
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 60/124,094
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/149,452
; PRIOR FILING DATE: 1999-08-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (33)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (197)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-116-166-6
Query Match 77.3%; Score 885.5; DB 9; Length 201;
Best Local Similarity 93.0%; Pred. No. 1.6e-86;
Matches 172; Conservative 2; Mismatches 8; Indels 3; Gaps 1;

34 KARGKQLKLIFFP---MSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQ 90
17 KKLGENNNLFFSPXXMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQ 76

QY 91 SLVAINRTDTEYVLTANGLFGEKSYDFTGTDSCGKGYQATIKQLDFVNDTEKSTTR 150
DB 77 SLVAINRTDTEYVLTANGLFGEKSYDFTGTDSCGKGYQATIKQLDFVNDTEKSTTR 136

QY 151 VNSWADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSIPKCNSPVTPHGMW 210
DB 137 VNSWADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSIPKCNSPVTPHGMW 196

QY 211 XPPSL 215
DB 197 XPPSL 201

RESULT 9
US-09-925-300-1440
; Sequence 1440, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1440
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-925-300-1440

Query Match 35.2%; Score 403.5; DB 10; Length 459;
Best Local Similarity 51.5%; Pred. No. 1.3e-34;
Matches 85; Conservative 29; Mismatches 36; Indels 15; Gaps 4;

34 KARGKQLKLIFFP---PMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSL 92
100 KTLGKDNKKNVFFSPMSMSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSL 158

QY 93 LVAINRTDTEYVLTANGLFGEKSYDFTGTDSCGKGYQATIKQLDFVNDTEKSTTRVN 152
DB 159 LTVNKTGTQYLLRMANRLFGEKSCDFLSSFRDSCQKPYQAEELDFISAVEKSRKHIN 218

QY 153 SWADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
DB 219 TWVAEKTEG-----KIAELLSFGSDVP-----LTELVLVNAV 250

RESULT 10
US-09-974-298-95
; Sequence 95, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hwei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
```


LENGTH: 41
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (37)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-912-628-13

Query Match 20.0%; Score 229; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 PGIASSCYCKACLSQPLLVHSHIPKCNSEVTPHGMWXPPL 215
Db 1 PGIASSCYCKACLSQPLLVHSHIPKCNSEVTPHGMWXPPL 41

RESULT 14

US-10-116-166-11
Sequence 11, Application US/10116166
Publication No. US20030040097A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT001P1
CURRENT APPLICATION NUMBER: US/10/116,166
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/641,721
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: PCT/US00/05092
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 60/122,276
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 60/124,094
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/149,452
PRIOR FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 41
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (37)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-116-166-11

Query Match 20.0%; Score 229; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 PGIASSCYCKACLSQPLLVHSHIPKCNSEVTPHGMWXPPL 215
Db 1 PGIASSCYCKACLSQPLLVHSHIPKCNSEVTPHGMWXPPL 41

RESULT 15

US-09-735-705-110
Sequence 110, Application US/09735705
Patent No. US2002052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 110
LENGTH: 391
TYPE: PRT
ORGANISM: Homo sapien
US-09-735-705-110

Query Match 19.6%; Score 224; DB 10; Length 391;
Best Local Similarity 32.7%; Pred. No. 1.5e-15;
Matches 53; Conservative 31; Mismatches 54; Indels 24; Gaps 4;

QY 38 KOLKQ-----LIFPPMSISSALAMVFMGAKGNTAAQMSQAL-----CFSKIGGEDGD-- 84
Db 17 KELKTNNDGNIFFPVGVILTAIGWLLGTRGATASQLEEVFHSSEKTSRRIKAEKEVI 76
QY 85 -----IHRGFQSLVAINRTDTTEYVLRNTANGLFGEKSYDELFTDSCGKGYOATIKOLD 139
Db 77 ENTEAVHQPFQKELTEISKLNDYELNITNRLFGEKTYLEFQKLYLDVVEKYHSLPEVD 136
QY 140 FVNDTEKSTTRVNSWADTKAWKIIQTSLSHLEEPGIASSS 181
Db 137 FVNADESRRKINSWESKT-----NEKIKDLFPDGSISS 172

Search completed: May 20, 2003, 10:35:38
Job time : 57 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: May 20, 2003, 10:22:17 ; Search time 44 Seconds
(without alignments)
469.748 Million cell updates/sec

Title: US-09-912-628-7
Perfect score: 1145
Sequence: 1 HELRSWAARRTGARRHGS.....SIPKCNPTVPHGMWPPSL 215
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404.5	35.3	376	1 A48681	placental thrombin
2	392.5	34.3	374	2 A59273	proteinase inhibit
3	370.5	32.4	378	2 A57488	proteinase inhibit
4	320	27.9	376	2 B59273	proteinase inhibit
5	272	23.8	390	2 I38202	leupin precursor -
6	266	23.2	390	2 I38201	squamous cell carc
7	257	22.4	379	2 A42421	leukocyte elastase
8	255.5	22.3	378	2 S38962	serpin - pig
9	240	21.0	379	2 S27383	elastase inhibitor
10	224	19.6	391	2 JC7118	headpin serine pro
11	221.5	19.3	415	2 A32853	plasminogen activa
12	216.5	18.9	415	2 S20047	plasminogen activa
13	213.5	18.6	397	2 I39184	bomapin - human
14	213	18.6	416	2 S19896	plasminogen activa
15	198.5	17.3	388	1 DYCH	ovalbumin-related
16	191.5	16.7	402	2 I49471	alpha-1 proteinase
17	190.5	16.6	413	2 I49452	alpha-1-antitrypsi
18	190.5	16.6	413	2 I49473	alpha-1 proteinase
19	189.5	16.6	413	2 I49474	alpha-1 proteinase
20	188.5	16.3	418	2 S23675	contrapsin-related
21	186.5	16.3	413	2 I49470	alpha-1 proteinase
22	186.5	16.3	413	2 I49472	alpha-1 proteinase
23	186.5	16.3	418	2 JH0494	alpha-1 antichymot
24	185	16.2	405	2 A35088	alpha-1-antitrypsi
25	185	16.2	406	2 JX0346	alpha-1-antitrypsi
26	184.5	16.1	418	2 JX0129	contrapsin precurs
27	184	16.1	418	2 A53120	intracellular coag
28	183.5	16.0	405	2 A28321	corticosteroid-bin
29	183.5	16.0	413	2 I56481	alpha-1-proteinase

30	183	16.0	410	2 C39088	contrapsin precurs
31	182	15.9	388	2 B39088	alpha-1-antitrypsi
32	181.5	15.9	411	1 ITRT	alpha-1-antitrypsi
33	181.5	15.9	417	2 S19724	kallikrein-binding
34	181	15.8	416	2 S21097	alpha-1-antitrypsi
35	179	15.6	413	2 A54968	alpha-1-antitrypsi
36	178.5	15.6	383	2 A36117	corticosteroid-bin
37	175	15.3	409	1 ITBA	alpha-1-antitrypsi
38	175	15.3	416	1 ITSH	alpha-1-antitrypsi
39	174	15.2	413	2 JX0267	alpha-1-antitrypsi
40	174	15.2	413	2 S54981	alpha-1-antitrypsi
41	173.5	15.2	408	2 S11320	serine proteinase
42	173.5	15.2	436	2 A42440	estrogen-regulated
43	173	15.1	413	2 JX0154	alpha-1-antitrypsi
44	170.5	14.9	418	1 S31507	serine proteinase
45	169	14.8	418	1 ITHU	alpha-1-antitrypsi

ALIGNMENTS

RESULT 1

A48681

placental thrombin inhibitor - human

N; Alternate names: cytoplasmic antiproteinase; intracellular serine proteinase inhibitor.

C: Species: Homo sapiens (man)

C: Date: 07-Apr-1994 #sequence revision 07-Jul-1995 #text change 18-Jun-1999

C: Accession: A48681; A54352; A46672; B46672; C46672; S35750

R: Coughlin, P.; Sun, J.; Cerruti, L.; Salem, H.H.; Bird, P.

Proc. Natl. Acad. Sci. U.S.A. 90, 9417-9421, 1993

A: Title: Cloning and molecular characterization of a human intracellular serine proteinase.

A: Reference number: A48681; MUID: 94022386; PMID: 8415716

A: Accession: A48681

A: Molecule type: mRNA

A: Residues: 1-376 <COU>

A: Cross-references: GB: Z22658; NID: 9297411; PIDN: CAA80373.1; PID: G297412

A: Experimental source: placenta

A: Note: authors translated the codon CAA for residue 198 as Gly

R: Morgenstern, K.A.; Sprecher, C.; Holch, L.; Foster, D.; Grant, F.J.; Ching, A.; Kisse

Biochemistry 33, 3432-3441, 1994

A: Title: Complementary DNA cloning and kinetic characterization of a novel intracellular

A: Reference number: A54352; MUID: 94183847; PMID: 8136380

A: Accession: A54352

A: Molecule type: mRNA

A: Residues: 1-174, 'E', 176-361, 'S', 363-376 <MOR>

A: Cross-references: GB: S69272; NID: 9546087; PIDN: AAB30320.1; PID: G546088

A: Experimental source: placenta

A: Note: sequence extracted from NCBI backbone (NCBIN: 145231, NCBIP: 145232)

R: Coughlin, P.B.; Tetaz, T.; Salem, H.H.

J. Biol. Chem. 268, 9541-9547, 1993

A: Title: Identification and purification of a novel serine proteinase inhibitor.

A: Reference number: A46672; MUID: 93252826; PMID: 8486644

A: Accession: A46672

A: Molecule type: protein

A: Residues: 47-60; 63-81; 91-98 <CO2>

A: Experimental source: placenta, leukemic cell line K562

A: Note: sequence modified after extraction from NCBI backbone

C: Genetics:

A: Gene: GDB: P16

A: Cross-references: GDB: 252025; OMIM: 173321

A: Map position: 6p25-6p24.3

C: Superfamily: antithrombin III

C: Keywords: blocked amino end; cytosol; serine proteinase inhibitor

F: 341/Inhibitory site: Arg (thrombin) #status predicted

Query Match 35.3%; Score 404.5; DB 1; Length 376;

Best Local Similarity 51.5%; Pred. No. 3.7e-30;

Matches 85; Conservative 29; Mismatches 36; Indels 15; Gaps 4;

QY 34 KARGKQLQLIFF-PWSTSSALAMVFMGKNTAQMCAQALCFKIGGEDGDIHQFQSL 92

DB 17 KTLGDKNSKNVFPSPMWSMCAAMVYMGKNTAQMCAQALCFKIGGEDGDIHQFQSL 75

93	Qy	LVA	INR	T	D	T	E	W	V	L	T	A	N	G	L	F	G	E	K	S	Y	D	E	L	T	G	F	T	D	S	C	G	F	Y	O	A	T	I	K	O	L	D	F	V	N	D	T	E	K	S	T	T	R	V	N	152	
76	Db	L	T	E	V	N	K	T	G	T	O	Y	L	L	R	V	A	N	L	F	G	E	K	S	C	D	F	L	S	F	R	S	C	O	F	Y	Q	A	E	M	E	L	D	F	I	S	A	V	E	K	S	R	K	H	I	N	135
153	Qy	S	W	A	D	K	T	K	A	W	K	I	I	O	T	S	L	H	E	E	P	G	I	A	S	S	S	C	Y	C	K	A	C	L	S	Q	P	L	V	H	S	I	197														
136	Db	T	W	A	E	K	T	E	G	-----	K	I	A	E	L	L	S	P	G	S	V	D	P	-----	L	T	R	L	V	L	N	A	V	167																							

RESULT 2

AS9273

proteinase inhibitor 8 - human

N;Alternate names: cytoplasmic antiproteinase 2 (CAP-2)

C;Species: Homo sapiens (man)

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C;Accession: A59273

R;Sprecher, C.A.; Morgenstern, K.A.; Mathewes, S.; Dahlen, J.R.; Schrader, S.K.; Foster, J. Biol. Chem. 270, 29854-29863, 1995

A;Title: Molecular cloning, expression, and partial characterization of two novel members of the proteinase inhibitor gene family

A;Reference number: A59273; MUID:96102099; PMID:8530382

A;Accession: A59273

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-374 <SPR>

A;Cross-references: GB:I40377; NID:g1160926; PIDN:AAC41939.1; PID:g1160927

A;Experimental source: tissue type placenta; note (vector lambda gt11; gene CAP2

C;Genetics:

A;Gene: GDB:PI8; CAP2

A;Cross-references: GDB:599392; OMIM:601697

A;Map position: 18q21.3-18q21.3

C;Superfamily: antithrombin III

C;Keywords: proteinase inhibitor

F:339/inhibitory site: Arg (unidentified proteinase) #status predicted

	Query Match	34.3%;	Score	392.5;	DB 2;	Length	374;			
	Best Local Similarity	52.9%;	Pred. No.	4.9e-29;						
	Matches	83;	Conservative	23;	Mismatches	34;	Indels	17;	Gaps	3;
Qy	41	KQLIFFPMSISSALAWPMGAKGNTAAQMSQALCFSGKIGGEDGDHIRGFQSLLVAINRTD	100	:	:	:	:	:	:	:
Dd	26	RNVFFSPMSISSALAWPMGAKGSTAAQMSQALCLYK-----DGDHIRGFQSLSEVNRGTG	81	:	:	:	:	:	:	:
Qy	101	TEYVLRTANGLFGBKSYDFLTGFTDCSCFKFYQATIKOLDVFNDTEKSTRVNSWVAOKT	160	:	:	:	:	:	:	:
Dd	82	TQYLRLTNANLFGEKTCDFLPDFKEYCQKFQAELSELSFAEDTEECRKHINDWAEKTE	141	:	:	:	:	:	:	:
Qy	161	AWKIQTSLSHLEPGIASSCCYKACUSQPLLVSII	197	:	:	:	:	:	:	:
Dd	142	G-----KISEVLDAGTVDP-----LTKLVNNAI	165	:	:	:	:	:	:	:

RESULT 3
A57488
proteinase inhibitor Sp13 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 16-Jul-1999
C:Accession: A57488
E:Sun, J.; Rose, J.B.; Bird, P.
J. Biol. Chem. 270, 16089-16096, 1995
A:Title: Gene structure, chromosomal localization, and expression of the murine homolog
A:Reference number: A57488; MUID:95332310; PMID:7608171
A:Accession: A57488
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SUN>
A:Cross-references: GB:U25844; NID:G818902; PIDN:AAA79684.1; PID:G818903
C:Genetics:
A:Gene: Sp13
A:Map position: 13
C:Superfamily: antithrombin III
C:Keywords: serine proteinase inhibitor
E:3347/Inhibitor site: Arg (unidentified proteinase) #status predicted

[illegible]

```

RESULT 4
B59273
proteinase inhibitor 9 - human
N;Alternate names: cytoplasmic antiproteinase 3 (CAP-3)
C;Species: Homo sapiens (man)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: B59273
R;Suppacher, C.A.; Morgenshtern, K.A.; Mathewes, S.; Dahlen, J.R.; Schrader,
J. Biol. Chem. 270, 29854-29861, 1995
A;Title: Molecular cloning, expression, and partial characterization of tw
A;Reference number: A59273; MUID:96102039; PMID:8530382
A;Accession: B59273
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-376 <SPR>
A;Cross-references: GB:I40378; NID:G1160928; PIDN:AAC41940.1; PID:gl160929
A;Experimental source: tissue type placenta; note (vector lambda gt11); ge
C;Genetics:
A;Gene: GDB:PI9; CAP3
A;Cross-references: GDB:599393; OMIM:601799
A;Map position: 6p25-6p25
C;Superfamily: antithrombin III
C;Keywords: proteinase inhibitor
P;340/inhibitory site: Glu (unidentified proteinase) #status predicted

```

	Query Match	27.9%;	Score 320;	DB 2;	Length 376;
	Best Local Similarity	46.3%;	Pred. No. 3.le-22;		
	Matches 68;	Conservative 28;	Mismatches 45;	Indels 6;	Gaps
Qy	47	PMSISSALAMVFVCAKNGNTAAQNSQALCFSGKIGDGDHHRGFQSLLVAINRRTDTEYVLR	106		
Db	32	PVSISSALAMVLLGAKNGNTATQWAQALSNL	---	TREDIHRAFGQSLLTENVKAGTQYLLR	87
Qy	107	TANLGFGEKSYDFLTGTGDCGKPYQATIKQLDFVNDTEKSTTRVNSVADKT	-	KAWKI	164
Db	88	TANLGFGEKTCQFLSTFKESCLOFYHAAELAKELSFIRAAEERKHINTVWSKKTGKIEEL	147		
Qy	165	IQTGLSHLEBFGFIASSCYCKACLSQP	191		
Db	148	LPGSSIDAETRLVLVNAIFYKGNWEP	174		

RESULT 5
I38202
leupin precursor - human
N:Alternate names: proteinase inhibitor 11 (Pill); squamous cell carcinoma
C:Species: Homo sapiens (man)
C:Date: 23-Feb-1996 #sequence revision 23-Feb-1996 #text_change 26-May-2000
C:Accession: I38202; S66675; S57522
R:Schneider, S.S.; Schick, C.; Fish, K.E.; Miller, E.; Pena, J.C.; Treter,
Proc. Natl. Acad. Sci. U.S.A. 92 3147-3151, 1995
A:Title: A serine proteinase inhibitor locus at 19q21.3 contains a tandem
A:Reference number: I38200; MUID:95241462; PMID:7724531
A:Accession: I38202
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA

A;Residues: 1-390 <SCH>
A;Cross-references: EMBL:U19576; GB:U19569; NID:g852466
R;Barnes, R.C.; Worrall, D.M.
FEBS Lett. 373, 61-65, 1995
A;Title: Identification of a novel human serpin gene; cloning sequencing and expression
A;Reference number: S66675; MUID:96013887; PMID:7589435
A;Accession: S66675
A;Molecule type: mRNA

A;Residues: 7-351,'V',353-384 <BAR>
A;Cross-references: EMBL:X89015; NID:g887464; PIDN:CAA61420.1; PID:g887465
C;Genetics:

A;Gene: GDB:SCCA2; P111

A;Cross-references: GDB:636556; OMIM:600518

A;Map position: 18q21.3-18q21.3

A;Introns: 55/3; 74/3; 117/3; 157/1; 204/3; 256/3

C;Superfamily: antithrombin III

C;Keywords: glycoprotein; serine proteinase inhibitor

F;1-22/Domain: signal sequence status predicted <SG>

F;33-384/Product: Leupin #status predicted <MAR>

F;65-93,170,376/Binding site: carbohydrate (Asn) #status predicted
F;354/Inhibitory site: Leu (unidentified proteinase) #status predicted

Query Match 23.8%; Score 272; DB 2; Length 390;
Best Local Similarity 38.6%; Pred. No. 1e-17;
Matches 54; Conservative 27; Mismatches 47; Indels 12; Gaps 1;

QY 32 FEKARGKQLKQLFFPMSISSALAMVFMGAKNTAAQMSQALCFKSG----- 79

DB 16 FQPRKSKENNIFYPSPISITSGALGMVLLGAKNTAAQIKKVLHFDQVTEITTKAATYHV 75

QY 80 GEDGDIHRGFSQSLVAINRTDTEVLTANGLFGEKSYDFLTGFTDSCGKFGYQATIKOLD 139

DB 76 DRSGNVHGFQKLLTFEKNSTDAYELKANKLFGEKTYLFQLEYLDAIKKFKYQTSVESTD 135

QY 140 FVNDTEKSTRVNSWADKT 159

DB 136 FANAPEESRKINSWESQT 155

RESULT 6

I38201

squamous cell carcinoma antigen 1 - human

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence revision 23-Feb-1996 #text_change 26-May-2000

C;Accession: I38201; I38200; G01631; J00967

R;Schneider, S.S.; Schick, C.; Fish, K.E.; Miller, E.; Pena, J.C.; Treter, S.D.; Hui, S.

Proc. Natl. Acad. Sci. U.S.A. 92, 3147-3151, 1995

A;Title: A serine proteinase inhibitor locus at 18q21.3 contains a tandem duplication of

A;Reference number: I38200; MUID:95241462; PMID:7724531

A;Accession: I38201

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-390 <SCH1>

A;Cross-references: EMBL:U19569; GB:U19558; NID:g1172085

A;Accession: I38200

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-117 <SCH2>

A;Cross-references: EMBL:U19562; NID:g897835; PIDN:AAA86316.1; PID:g897844

R;Silverman, G.A.

submitted to the EMBL Data Library, January 1995

A;Reference number: G07968

A;Accession: G01631

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-350,'G',352-390 <SLU>

A;Cross-references: EMBL:U19556; NID:g1276435; PID:g1052869

R;Suminami, Y.; Kishi, F.; Sekiguchi, K.; Kato, H.

Biochem. Biophys. Res. Commun. 181, 51-58, 1991

A;Title: Squamous cell carcinoma antigen is a new member of the serine protease inhibitor

A;Reference number: J00966; MUID:92068241; PMID:1958219

A;Accession: J00966

A;Molecule type: mRNA

A;Residues: 1-350,'G',352-356,'A',358-390 <SUM1>
A;Cross-references: GB:S66896; NID:g239551; PIDN:AAB20405.1; PID:g239552
A;Accession: J00967

A;Molecule type: protein

A;Residues: 11-21,231-237;240-256;303-325 <SUM2>

C;Comment: This antigen probably acts as a proteinase inhibitor to modulate the host i

C;Genetics:

A;Gene: GDB:SCCA1; SCC

A;Cross-references: GDB:625364; OMIM:600517

A;Map position: 18q21.3-18q21.3

A;Introns: 55/3; 74/3; 117/3; 157/1; 204/3; 256/3

C;Superfamily: antithrombin III

C;Keywords: cysteine proteinase inhibitor; glycoprotein

F;65-93,171,376/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;354/Inhibitory site: Ser (cathepsin L) #status predicted

Query Match 23.2%; Score 266; DB 2; Length 390;

Best Local Similarity 37.9%; Pred. No. 3.8e-17;

Matches 53; Conservative 28; Mismatches 47; Indels 12; Gaps 1;

QY 32 FEKARGKQLKQLFFPMSISSALAMVFMGAKNTAAQMSQALCFKSG----- 79

DB 16 FQPRKSKENNIFYPSPISITSGALGMVLLGAKNTAAQIKKVLHFDQVTEITTKAATYHV 75

QY 80 GEDGDIHRGFSQSLVAINRTDTEVLTANGLFGEKSYDFLTGFTDSCGKFGYQATIKOLD 139

DB 76 DRSGNVHGFQKLLTFEKNSTDAYELKANKLFGEKTYLFQLEYLDAIKKFKYQTSVESVD 135

QY 140 FVNDTEKSTRVNSWADKT 159

DB 136 FANAPEESRKINSWESQT 155

RESULT 7

A42421

leukocyte elastase inhibitor - horse

N;Alternate names: plasminogen activator inhibitor-2 homolog

C;Species: Equus caballus (domestic horse)

C;Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 02-Jun-2000

C;Accession: A42421; A37276; S34062

R;Dubin, A.; Travis, J.; Enghild, J.J.; Potempa, J.

J. Biol. Chem. 267, 6576-6583, 1992

A;Title: Equine leukocyte elastase inhibitor. Primary structure and identification as a

A;Reference number: A42421; MUID:92202200; PMID:1551869

A;Accession: A42421

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-379 <DUB1>

A;Cross-references: PIDN:AAB21885.1; PID:g247842

A;Experimental source: leukocyte

A;Note: sequence extracted from NCBI backbone (NCBI:89849)

R;Dubin, A.; Travis, J.; Enghild, J.J.; Potempa, J.

submitted to the Protein Sequence Database, December 1991

A;Reference number: A37276

A;Accession: A37276

A;Molecule type: protein

A;Residues: 1-41,'E',43-325,'VD',326-379 <DUB2>

R;Kordula, T.; Dubin, A.; Schooltink, H.; Koj, A.; Heinrich, P.C.; Rose-John, S.

Biochem. J. 293, 187-193, 1993

A;Title: Molecular cloning and expression of an intracellular serpin: an elastase inhib

A;Reference number: S34062; MUID:93319507; PMID:7687128

A;Accession: S34062

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-379 <KOR>

A;Cross-references: GB:M91161; NID:g164240; PIDN:AAA97513.1; PID:g164241

C;Superfamily: antithrombin III

C;Keywords: serine proteinase inhibitor

Query Match 22.4%; Score 257; DB 2; Length 379;

Best Local Similarity 46.5%; Pred. No. 2.6e-16;

Matches 53; Conservative 19; Mismatches 38; Indels 4; Gaps 1;

Wed May 28 14:44:10 2003

us-09-912-628-7.rpr

Query Match 21.0%; Score 240; DB 2; Length 379;
Best Local Similarity 43.0%; Pred. No. 1e-14;
Matches 49; Conservative 23; Mismatches 38; Indels 4; Gaps 1;
QY 47 PMSISSALAMVFMGAKGNTAAQMSQALCFKSGIGEDGDIHRGFSQSLLVAINRTDTEYVLR 106
DB 32 PLSISSALAMIFLGRGNTAAQVSKALYFDTV---EDHRSFQSLNADINKPGAPYLK 87
QY 107 TANGLFGEKSYDFLTGTDCGKGYQATIKQLDFVNDTEKSTTRVNSWVADTK 160
DB 88 LANRLYGEKTYNFLADFLASTQKMGAEASVDVFPQAPEDARKINEWVGQTE 141
RESULT 8
S38962
serpin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Jul-1998
C:Accession: S38962
R:Teuchauer, W.F.; Mentelle, R.; Sommerhoff, C.P.
Eur. J. Biochem. 217, 519-526, 1993
A:Title: Primary structure of a porcine leukocyte serpin.
A:Reference number: S38962; MUID:94039085; PMID:7901009
A:Accession: S38962
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-378 <TFS>
A:Note: the sequence from Fig. 6 is inconsistent with that from Fig. 5 in having 256-Asn
C:Superfamily: antithrombin III
Query Match 22.3%; Score 255.5; DB 2; Length 378;
Best Local Similarity 39.1%; Pred. No. 3.6e-16;
Matches 59; Conservative 27; Mismatches 48; Indels 17; Gaps 3;
QY 47 PMSISSALAMVFMGAKGNTAAQMSQALCFKSGIGEDGDIHRGFSQSLLVAINRTDTEYVLR 106
DB 32 PFSISSALAMILLGRGNTAAQMSKALHFDTV---KDIHRSFQSLNADINKGASYLK 87
QY 107 TANGLFGEKSYDFLTGTDCGKGYQATIKQLDFVNDTEKSTTRVNSWVADTKAWKIIQ 166
DB 88 LANRLYGEKTYHFLPEFLASTQKTYGAELASVDVFLRASEEARKAINWVKQTEG----- 142
QY 167 TSLSHLEBPGIASSCYKACLSQBLVHSI 197
DB 143 -KIPELLASGVVDSA-----TKLVLVNAI 165
RESULT 9
S27383
elastase inhibitor - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Sep-1997
C:Accession: S27383; S65750
C:Superfamily: S27383
A:Title: Sequence and molecular characterization of human monocyte/neutrophil elastase
A:Reference number: S27383; MUID:92302296; PMID:1376927
A:Accession: S27383
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-379 <REM>
A:Cross-references: EMBL:M93056
R:Packard, B.Z.; Lee, S.S.; Remold-O'Donnell, E.; Komoriya, A.
Biochim. Biophys. Acta 1269, 41-50, 1995
A:Title: A serpin from human tumor cells with direct lymphoid immunomodulatory activity.
A:Reference number: S65750; MUID:96049524; PMID:7578269
A:Accession: S65750
A:Status: preliminary
A:Molecule type: protein
A:Residues: 57-69; 97-110; 111-129; 204-213; 216-244; 255-271, 'X', 273-274; 291-301 <PAC>
C:Genetics:
A:Gene: GDB:ELANH2; EI; P12
A:Cross-references: GDB:132914; OMIM:130135
A:Map position: 6p25-6p24.3
C:Superfamily: antithrombin III
C:Keywords: serine proteinase inhibitor

Query Match 21.0%; Score 240; DB 2; Length 379;
Best Local Similarity 43.0%; Pred. No. 1e-14;
Matches 49; Conservative 23; Mismatches 38; Indels 4; Gaps 1;
QY 47 PMSISSALAMVFMGAKGNTAAQMSQALCFKSGIGEDGDIHRGFSQSLLVAINRTDTEYVLR 106
DB 32 PFSISSAMAVFLGRGNTAAQLSKTFHTV---EEVHSRFQSLNADINKRGASYILK 87
QY 107 TANGLFGEKSYDFLTGTDCGKGYQATIKQLDFVNDTEKSTTRVNSWVADTK 160
DB 88 LANRLYGEKTYNFLPEFLVSTOKTYCADLASVDVFOHASEDARKTINQWVGQTE 141
RESULT 10
JC7118
headpin serine proteinase inhibitor - human
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 26-May-2000
C:Accession: JC7118
R:Spring, P.; Nakashima, T.; Frederick, M.; Henderson, Y.; Clayman, G.
Biochem. Biophys. Res. Commun. 264, 299-304, 1999
A:Title: Identification and cDNA cloning of headpin, a novel differentially expressed s
A:Reference number: JC7118; MUID:99458661; PMID:10527881
A:Accession: JC7118
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-391 <SPR>
A:Cross-references: GB:AF169949; NID:G5911368; PIDN:AAD55765.1; PID:G5911369
C:Genetics:
A:Map position: 18q21.3-18q22
C:Superfamily: antithrombin III
C:Keywords: serine proteinase inhibitor
P:355/Inhibitory site: Val (unidentified proteinase) #status predicted
Query Match 19.6%; Score 224; DB 2; Length 391;
Best Local Similarity 32.7%; Pred. No. 3.4e-13;
Matches 53; Conservative 31; Mismatches 54; Indels 24; Gaps 4;
QY 38 KOLKQ-----LIFFPMSISSALAMVFMGAKGNTAAQMSQAL-----CFSKIGEGDGD-- 84
DB 17 KELKTNIDGNIFPSPVIGILTAIMGVLVLTGRGATASQLEEVFHSSEKTSRKIAKEEVI 76
QY 85 -----IHRGFSQSLLVAINRTDTEYVLTANGLFGEKSYDFLTGTDCGKGYQATIKOLD 139
DB 77 ENTEAVHQFQKFLTEISKLTNDYELNITNRLFGKTYLFLQKLYDVEKYYHASLEPVD 136
QY 140 FVNDTEKSTTRVNSWVADTKAWKIIQTSLSHLEEPGIASSS 181
DB 137 FVNADESRRKINSWVESKT-----NEKIKOLFPPDGSISSS 172
RESULT 11
A32853
plasminogen activator inhibitor 2 precursor - human
N:Alternate names: urokinase inhibitor
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 20-Oct-2000
C:Accession: A32853; I54218; A31366; A46543; A29362; A53815; A25021; S02435; I5.
R:Ye, R.D.; Ahern, S.M.; Le Beau, M.M.; Lebo, R.V.; Sadler, J.E.
J. Biol. Chem. 264, 5495-5502, 1989
A:Title: Structure of the gene for human plasminogen activator inhibitor-2. The nearest
A:Reference number: A32853; MUID:89174589; PMID:2494165
A:Accession: A32853
A:Molecule type: DNA
A:Residues: 1-415 <YER>
A:Cross-references: GB:M24651; GB:M24652; GB:M24653; GB:M24654; GB:M24655; GB:M24656; I5.
R:Samia, J.A.; Alexander, S.J.; Horton, K.W.; Auron, P.E.; Byers, M.G.; Shows, T.B.
Genomics 6, 159-167, 1990
A:Title: Chromosomal organization and localization of the human urokinase inhibitor gen
A:Reference number: I54218; MUID:90152678; PMID:2303256
A:Accession: I54218
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA

A;Residues: 1-415 <RES>
A;Cross-references: GB:M31551; NID:G340152; PIDN:AAA36797.1; PID:G340154
R;Antalis, T.M.; Clark, M.A.; Barnes, T.; Lehrbach, P.R.; Devine, P.L.; Schvezov, G.; G
Proc. Natl. Acad. Sci. U.S.A. 85: 985-989, 1988
A;Title: Cloning and expression of a cDNA coding for a human monocyte-derived plasminoge
A;Reference number: A31366; MUID:88125032; PMID:3257578
A;Accession: A31366
A;Molecule type: mRNA
A;Residues: 1-415 <ANT>
A;Cross-references: GB:J03603; NID:G189546; PIDN:AAA60004.1; PID:G189547
R;Webb, A.C.; Collins, K.L.; Snyder, S.E.; Alexander, S.J.; Rosenwasser, L.J.; Eddy, R.I
J. Exp. Med. 166, 77-94, 1987
A;Title: Human monocyte Arg-serpin cDNA. Sequence, chromosomal assignment, and homology
A;Reference number: A46543; MUID:87252928; PMID:3496414
A;Accession: A46543
A;Molecule type: mRNA
A;Residues: 1-415 <WEB>
A;Cross-references: GB:Y00630; NID:G35267; PIDN:CAA68666.1; PID:G35268
R;Schleuning, W.D.; Medcalf, R.L.; Hession, C.; Rothenbuehler, R.; Shaw, A.; Kruithof, E
Cell. Biol. 7, 4564-4567, 1987
A;Title: Plasminogen activator inhibitor 2: regulation of gene transcription during pho
A;Reference number: A29362; MUID:88142852; PMID:3325828
A;Accession: A29362
A;Molecule type: mRNA
A;Residues: 1-119, D', 121-403, K', 405-412, C', 414-415 <SCH>
A;Cross-references: GB:M18082; NID:G189562; PIDN:AAA60006.1; PID:G189563
R;Ye, R.D.; Wun, T.C.; Sadler, J.E.
J. Biol. Chem. 262, 3718-3725, 1987
A;Title: cDNA cloning and expression in Escherichia coli of a plasminogen activator inh
A;Reference number: A26553; MUID:87137674; PMID:3029122
A;Accession: A26553
A;Molecule type: mRNA
A;Residues: 1-119, D', 121-403, K', 405-412, C', 414-415 <YE2>
A;Cross-references: GB:J02685; NID:G189544; PIDN:AAA6413.1; PID:G189545
A;Experimental source: placenta
R;Jensen, P.H.; Schueler, E.; Woodrow, G.; Richardson, M.; Goss, N.; Hojrup, P.; Peterse
J. Biol. Chem. 269, 15394-15398, 1994
A;Title: A unique interhelical insertion in plasminogen activator inhibitor-2 contains t
A;Reference number: A53815; MUID:94253109; PMID:7910824
A;Accession: A53815
A;Molecule type: protein
A;Residues: 83-87 <JEN>
R;Kruithof, E.K.O.; Vassalli, J.D.; Schleuning, W.D.; Mattaliano, R.J.; Bachmann, F.
J. Biol. Chem. 261, 11207-11213, 1986
A;Title: Purification and characterization of a plasminogen activator inhibitor from the
A;Reference number: A25021; MUID:86278222; PMID:3090045
A;Accession: A25021
A;Molecule type: protein
A;Residues: 347-376 <KRU>
R;Kiso, U.; Kaudewitz, H.; Henschen, A.; Aetted, B.; Kruithof, E.K.O.; Bachmann, F.
FEBS Lett. 230, 51-56, 1988
A;Title: Determination of intermediates, products and cleavage site in the reaction betw
A;Reference number: S02435; MUID:88167197; PMID:3280346
A;Accession: S02435
A;Molecule type: protein
A;Residues: 377-415 <KIS>
R;Kruithof, E.K.; Cousin, E.
Biochem. Biophys. Res. Commun. 156, 383-388, 1988
A;Title: Plasminogen activator inhibitor 2. Isolation and characterization of the promot
A;Reference number: I52229; MUID:89025873; PMID:2845977
A;Accession: I52229
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-56 <RE2>
A;Cross-references: GB:M23092; NID:G189559; PIDN:AAA60005.1; PID:G189561
C;Genetics:
A;Gene: GDB:PA12; PLANH2
A;Cross-references: GDB:120298; OMIM:173390
A;Map position: 18q21.2-18q22
A;Intons: 56/3; 96/3; 139/3; 179/1; 226/3; 281/3
C;Superfamily: antithrombin III
A;Keywords: acetylated amino end; glycoprotein; serine proteinase inhibitor
P;1-22/Domain: signal sequence #status predicted <SIG>

F;23-415/Product: plasminogen activator inhibitor 2 #status predicted <MAT>
F;23/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
F;75.115.339/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;83.84.86/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of unidentified prot
F;380-381/Cleavage site: Arg-Thr (plasminogen activator) #status experimental
F;380/Inhibitory site: Arg (plasminogen activator) #status experimental
Query Match 19.3%; Score 221.5; DB 2; Length 415;
Best Local Similarity 32.1%; Pred. No. 6.2e-13;
Matches 51; Conservative 27; Mismatches 48; Indels 33; Gaps 2;
QY 35 ARGKQLKQLIFPMPMISSALAMVFMGAKGNTAAQMSQALCFSGKIG----- 79
DB 20 AKASPTQNLFLSPWISSTTMAMVYMGSGRSTEDQNAKVLQFNEVGANAVTPMTPEFTSC 79
QY 80 -----GEDGD-----IHRGFQSLVAINRTDTEYVLTANGLFGEKSYDFLT 121
DB 80 GFMOQIQKGYSDPAILOQAADKIHSSFRSLSSAINASTGNLYLSEVKNLFGEKSASPRE 139
QY 122 GFTDSCGFYQATIKQLDFVNDTEKSTTRVNSWADKTK 160
DB 140 EYRLCQKYSEPOAVDFLECAEAREKINSWVKTQTK 178
RESULT 12
S20047
Plasminogen activator inhibitor 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C;Accession: S20047; S09616
R;Belin, D.
submitted to the EMBL Data Library, September 1989
A;Reference number: S20047
A;Accession: S20047
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-415 <BEL>
A;Cross-references: EMBL:X16490; NID:G53589; PIDN:CAA34507.1; PID:G53590
R;Belin, D.; Wohlwend, A.; Schleuning, W.D.; Kruithof, E.K.O.; Vassalli, J.D.
EMBO J. 8, 3287-3294, 1989
A;Title: Facultative polypeptide translocation allows a single mRNA to encode the secret
A;Reference number: S09615; MUID:90059920; PMID:2583099
A;Accession: S09616
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-27 <BEL2>
A;Cross-references: EMBL:X16490
C;Superfamily: antithrombin III
Query Match 18.9%; Score 216.5; DB 2; Length 415;
Best Local Similarity 32.7%; Pred. No. 1.8e-12;
Matches 54; Conservative 23; Mismatches 53; Indels 35; Gaps 3;
QY 29 IKPFKARGKQLKQLIFPMPMISSALAMVFMGAKGNTAAQMSQALCFSGKIG----- 79
DB 16 LKQIEKSNSTQ--NIFISPWISSTLTALVILGAGNTQQMAKVLQFNEIGSYGITRNP 73
QY 80 -----GEDGD-----IHRGFQSLVAINRTDTEYVLTANGLFGEK 115
DB 74 ENFGCDPAQIQKENVPSAILQQAQDKIHSFSSLSSTINTPGDYLLSEANKLFGEK 133
QY 116 SYDFLTGFTDSCGFYQATIKQLDFVNDTEKSTTRVNSWADKTK 160
DB 134 SARFKEEYQLSKKYSTEPEAVDFLECAEAREKINSWVKTQTK 178
RESULT 13
I39184
bomapin - human
N;Alternate names: proteinase inhibitor 10 (PI10)
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 16-Jul-1999
C;Accession: I39184

Nucleic Acids Res. 10, 4363-4382, 1982
A:Title: The ovalbumin gene family: complete sequence and structure of the Y gene.
A:Reference number: A01244; MUID:83014329; PMID:7122240
A:Accession: A01244
A:Molecule type: DNA
A:Residues: 1-388 <HEI>
A:Cross-references: GB:J00922; GB:V00439; NID:g212899; PIDN:AAA68882.1; PID:g212900
C:Genetics:
A:Introns: 56/3; 73/3; 116/3; 156/1; 203/3; 255/3
C:Superfamily: antithrombin III
C:Keywords: glycoprotein; phosphoprotein; serine proteinase inhibitor
F:74-121/Disulfide bonds: #status predicted
P:293/Binding site: carboxylate (Asn) (covalent) #status predicted
P:345/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 17.3%; Score 198.5; DB 1; Length 389;
Best Local Similarity 30.1%; Pred. No. 8.3e-11;
Matches 43; Conservative 32; Mismatches 57; Indels 11; Gaps 2;

QY 28 CIKPEKARGKQLKQ-LIFFPMSISSALAMVFMGAKGNTAAQMSQALCFKSGEDGD-- 84
Db 12 CFDEVENEMKVHVHVNENILYCPLSILITAMVYLGAAGNTESQMKVLFHDSITGAGSTTD 71
QY 85 -----IHRGFQSLVAINRTDTEYVLRVLTANGLFGEKSYDFLTGFTDSCGKFFQATIK 136
Db 72 SQCGSSEYVHNLFKELLSEITRPNATYSLEIADKLYVDKTFVSLPEYLSCAKRFYTGVE 131
QY 137 QLDVNDTEKSTTRVNSWADKT 159
Db 132 EYVNTAAEEARQLINSWVERET 154

Search completed: May 20, 2003, 10:26:44
Job time : 46 secs

R:Riewald, M.; Schleef, R.R.
J. Biol. Chem. 270, 26754-26757, 1995
A:Title: Molecular cloning of bomapin (potease inhibitor 10), a novel human serpin that
A:Reference number: I39184; MUID:96070759; PMID:7592909
A:Accession: I39184
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-397 <RES>
A:Cross-references: EMBL:U35459; NID:g1065409; PIDN:AAC50282.1; PID:g1065409
C:Genetics:
A:Gene: GDB:P110
A:Cross-references: GDB:636283
A:Map position: 14q32.1-14q32.1
C:Superfamily: antithrombin III
C:Keywords: serine proteinase inhibitor

Query Match 18.6%; Score 213.5; DB 2; Length 397;
Best Local Similarity 32.2%; Pred. No. 3.3e-12;
Matches 47; Conservative 34; Mismatches 44; Indels 21; Gaps 2;

QY 33 EKARGKQLKQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFKSGIGG----- 80
Db 21 ESAQG---KNIPFSSISITSLTIVLGAQTAAQMAQVLFQFNDRDQGVKCDPESEKKRK 77
QY 81 -----EDGDIHRGFQSLVAINRTDTEYVLRVLTANGLFGEKSYDFLTGFTDSCGKFFQAT 134
Db 78 MEFNLNSEIHSDFQTLSEILKPNDDVLLKTANAIYGEKTYAFHNKYLEDMKTYFGAE 137
QY 135 IKOLDFVNDTEKSTTRVNSWADKTK 160
Db 138 PQPVNFEASDQIRKINSWVERQTE 163

RESULT 14
S19896
plasminogen activator inhibitor 2 type A - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C:Accession: S19896
R:Grundmann, U.; Rein, T.
A:Description: Complete cDNA sequence encoding plasminogen activator inhibitor 2 type A
submitted to the EMBL Data Library, February 1992
A:Reference number: S19896
A:Accession: S19896
A:Molecule type: mRNA
A:Residues: 1-416 <GRU>
A:Cross-references: EMBL:X64563; NID:g56834; PIDN:CAA45864.1; PID:g56835
C:Superfamily: antithrombin III

Query Match 18.6%; Score 213; DB 2; Length 416;
Best Local Similarity 31.9%; Pred. No. 3.9e-12;
Matches 53; Conservative 22; Mismatches 55; Indels 36; Gaps 3;

QY 29 IKPEKARGKQLKQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFKSGIGG----- 82
Db 16 LKQIEQNSNQ--NIFISPSNISLAIIVLGAQNTAEQMAKVLNEDKIGSYDLTPGNP 73
QY 83 -----GDHIFQSLVAINRTDT--EYVLRVLTANGLFGE 114
Db 74 ENFHGCDFAHQIRDNYFVAILQAQRDKIHSAFSSLSSTINTPRLDGVLLESANKLFGE 133
QY 115 KSYDPLTGFTDSCGKFFQATIKOLDVNDTEKSTTRVNSWADKTK 160
Db 134 KSARFKEEYIQRCKKYSTEPEAVDFLECANEARAKKINSWVKQTQK 179

RESULT 15
DYCH
ovalbumin-related Y protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 18-Jun-1999
C:Accession: A01244
R:Heilig, R.; Muraskowsky, R.; Kloepper, C.; Mandel, J.L.

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2003, 10:19:11 ; Search time 13 Seconds
(without alignments)
685.955 Million cell updates/sec

Title: US-09-912-628-7

Perfect score: 1145

Sequence: 1 HELRSWAAARRTGARRHGCS.....SIPKCNSPVTPHGMXPPSL 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Spaced: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	404.5	35.3	376	1 PT16 HUMAN	P35237 homo sapien
2	392.5	34.3	374	1 SPB8 HUMAN	P50452 homo sapien
3	388	33.9	378	1 PT16 BOVIN	O02739 bos taurus
4	370.5	32.4	378	1 PT16 MOUSE	Q60854 mus musculus
5	370	32.4	376	1 SPB9 HUMAN	P50453 homo sapien
6	272	23.8	390	1 SCC2 HUMAN	P48594 homo sapien
7	266	23.2	390	1 SCC1 HUMAN	P29508 homo sapien
8	257	22.4	379	1 ILEU HORSE	P05619 equus caball
9	255.5	22.3	378	1 ILEU PIG	P80229 sus scrofa
10	240	21.0	379	1 ILEU HUMAN	P30740 homo sapien
11	224	19.6	391	1 SB13 HUMAN	Q9uiv8 homo sapien
12	221.5	18.3	415	1 PA12 HUMAN	P05120 homo sapien
13	216.5	18.9	415	1 PA12 MOUSE	P12388 mus musculus
14	213.5	18.6	397	1 SB10 HUMAN	P48595 homo sapien
15	213	18.6	416	1 PA12 RAT	P29524 rattus norv
16	207	18.1	413	1 ALST TAMST	O54760 tamias sibi
17	202	17.6	413	1 ALST TAMST	O54759 tamias sibi
18	198.5	17.3	388	1 OVAY CHICK	O54757 tamias sibi
19	197	17.2	413	1 ALUM TAMST	O90955 tamias sibi
20	196	17.1	392	1 SB11 HUMAN	Q96p63 homo sapien
21	196	17.1	413	1 HP55 TAMST	O54758 tamias sibi
22	193.5	16.9	405	1 SB12 HUMAN	P22599 mus musculus
23	193	16.9	413	1 ALMS TAMST	Q00897 mus musculus
24	190.5	16.6	413	1 ALT2 MOUSE	Q00897 mus musculus
25	190.5	16.6	413	1 ALT4 MOUSE	Q00898 mus musculus
26	189.5	16.6	413	1 ALT5 MOUSE	P07758 mus musculus
27	186.5	16.3	413	1 ALT1 MOUSE	Q00898 mus musculus
28	186.5	16.3	413	1 ALT3 MOUSE	Q00898 mus musculus
29	185	16.2	405	1 ALAS CAVPO	P22325 cavia porce
30	184.5	16.1	418	1 COTR MOUSE	P07759 mus musculus
31	183.5	16.0	405	1 CSB HUMAN	P08185 mus sapien
32	183	16.0	410	1 COTR CAVPO	P22323 cavia porce
33	181.5	15.9	411	1 ALAT RAT	P17475 rattus norv

34	181.5	15.9	417	1 KBP MOUSE	P29621 mus musculus
35	181	15.8	403	1 ALAF CAVPO	P22324 cavia porce
36	181	15.8	416	1 ALAT BOVIN	P34955 bos taurus
37	180	15.7	412	1 ALAT CALCN	O54763 callosciuru
38	178.5	15.6	383	1 CSB RABIT	P23775 cryctolagus
39	178.5	15.6	418	1 CPI6 RAT	P09006 rattus norv
40	175	15.3	380	1 SPB7 HUMAN	O75635 homo sapien
41	175	15.3	409	1 ALAT PAPAN	P01010 papio anubi
42	175	15.3	416	1 ALAT SHEEP	P12725 ovila aries
43	173.5	15.2	436	1 EP45 XENLA	O00387 xenopus lae
44	173	15.1	413	1 ALAF RABIT	P23035 cryctolagus
45	170.5	14.9	418	1 S124 APOSY	Q60396 apodemus ay

ALIGNMENTS

RESULT 1

PT16 HUMAN
ID PT16 HUMAN STANDARD; PRT; 376 AA.
AC P35237; Q96J44;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Placental thrombin inhibitor (Cytoplasmic antiproteinase) (CAP)
DE (Protease inhibitor 6) (PI-6).
GN SERPINB6 OR PI6 OR PTI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94022386; PubMed=8415716;
RA Coughlin P., Sun J., Cerruti L., Salem H.H., Bird P.;
RT "Cloning and molecular characterization of a human intracellular
serine proteinase inhibitor";
RL Proc. Natl. Acad. Sci. U.S.A. 90:9417-9421(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 67-73 AND 144-149.
RC TISSUE=Placenta;
RX MEDLINE=94183847; PubMed=8136380;
RA Morgenstern K.A., Sprecher C.A., Holth L., Foster D., Grant F.J.,
Ching A., Kisiel W.;
RT "Complementary DNA cloning and kinetic characterization of a novel
intracellular serine proteinase inhibitor: mechanism of action with
trypsin and factor Xa as model proteinases";
RL Biochemistry 33:3432-3441(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX Strausberg R.;
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Inhibits thrombin.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN SKELETAL MUSCLE. ALSO FOUND
IN PLACENTA, CARDIAC MUSCLE, LUNG, LIVER, KIDNEY AND PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
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CC EMBL; Z22658; CAA80373.1; -
CC EMBL; S69272; AAB30320.1; -
CC EMBL; BC001394; AAH01394.1; -
CC PIR; S35750; S35750.
CC PIR; A48681; A48681.

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EMBL; D55670; BAA19875.1; --
HSP; P05120; 1BY7.
InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Serpin, Serine protease inhibitor.
ACT_SITE 341 342
E -> G (IN REF. 1).
CONFLICT 175 176
S -> R (IN REF. 1).
CONFLICT 362 363
SEQUENCE 376 AA; 42590 MW; 2B46A55F40C608C6 CRC64;

Query Match 35.3%; Score 404.5; DB 1; Length 376;
Best Local Similarity 51.5%; Pred. No. 5.6e-31;
Matches 85; Conservative 29; Mismatches 36; Indels 15; Gaps 4;

QY 34 KARGKOLKLIFF-PMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGDDIHRGFQSL 92
D 17 KTLGKDNISNVPFSPMSKALAMVFMGAKGNTAAQMAQLISFNKSGG-GGDIHQFQSL 75
Q 93 LVAINRTDEYLVRTANGLFGEKSYDFLTGTDSCGKGYQATIKQLDFVNDTEKSTRVN 152
D 76 LTVNKIGTQYLLRVANRLFGEKSCDFLSSFRDSCQKPYQAEEMELDFISAVEKSRKHIN 135
QY 153 SWVADTKKAWKIQTSLSHLEPGIASSCYKACLSQPLLVHSI 197
D 136 TWAVENTEG-----KIAELLSFGSDVP-----LTLELVLVNAV 167

RESULT 2
SPB8_HUMAN STANDARD; PRT; 374 AA.
ID SPB8_HUMAN
AC P50452;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytoplasmic antiprotease 2 (CAP2) (CAP-2) (Protease inhibitor 8) (Serpin B8).
DE SERPINB8 OR P18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96102039; PubMed=8530382;
PT Schrader S.K., Morgenstern K.A., Mathewes S., Dahlen J.R., Schradner S.K., Foster D.C., Kiesel W.;
KW "Molecular cloning, expression, and partial characterization of two novel members of the ovalbumin family of serine proteinase inhibitors";
RL J. Biol. Chem. 270:29854-29861(1995).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.

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EMBL; L40377; AAC41939.1; --
HSP; P05120; 1BY7.
Genew; HGNC:8952; SERPINB8.
InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.

Query Match 33.9%; Score 388; DB 1; Length 378;
Best Local Similarity 60.8%; Pred. No. 2.1e-29;
Matches 73; Conservative 21; Mismatches 26; Indels 0; Gaps 0;

QY 41 KQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGDDIHRGFQSLVAINRTD 100

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EMBL; D55670; BAA19875.1; --
HSP; P05120; 1BY7.
InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Serpin, Serine protease inhibitor.
ACT_SITE 343 344
SEQUENCE 378 AA; 42560 MW; 664F499CCFCE263A CRC54;

Query Match 33.9%; Score 388; DB 1; Length 378;
Best Local Similarity 60.8%; Pred. No. 2.1e-29;
Matches 73; Conservative 21; Mismatches 26; Indels 0; Gaps 0;

QY 41 KQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGDDIHRGFQSLVAINRTD 100

RESULT 5

SPB9_HUMAN

ID SPB9_HUMAN STANDARD; PRT; 376 AA.

AC P50453;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Cytoplasmic antiprotease 3 (CAP3) (CAP-3) (Protease inhibitor 9)

DE (Serpin B9).

GN SERPINB9 OR P19.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=96102039; PubMed=8530382;

RA Sprecher C.A., Morgenstern K.A., Mathewes S., Dahlen J.R.,

RA Schrader S.K., Foster D.C., Kiesel W.,

RT "Molecular cloning, expression, and partial characterization of two

RT novel members of the ovalbumin family of serine proteinase

RT inhibitors.";

RL J. Biol. Chem. 270:29854-29861(1995).

[2]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta, and Bone marrow;

RX MEDLINE=97066975; PubMed=8910377;

RA Sun J., Bird C.H., Sutton V., McDonald L., Coughlin P.B., Jong T.A.

RA Trapani J.A., Bird P.I.;

RT "A cytosolic granzyme B inhibitor related to the viral apoptotic

RT regulator cytokine response modifier A is present in cytotoxic

RT lymphocytes.";

RL J. Biol. Chem. 271:27802-27809(1996).

[3]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: GRANZYME B INHIBITOR.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.

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CC or send an email to license@ebi.ac.uk.

DR EMBL; L40378; AAC41940.1; -

DR EMBL; U71364; AAC50793.1; -

DR EMBL; BC002538; AAH02538.1; -

DR HSSP; P05120; 1BY7.

DR Genew; HGNC:8955; SERPINB9.

DR MIM; 601799;

DR InterPro; IPR000215; Serpin.

DR Pfam; PF00079; serpin; 1.

DR SMART; SM00093; SERPIN; 1.

DR PROSITE; PS00284; SERPIN; 1.

DR Serpin; Serine protease inhibitor.

FW ACT SITE 340 341

KT SEQUENCE 376 AA; 42403 MW; ECBAB0869B939753 CRC64;

SQ

Query Match 27.9%; Score 320; DB 1; Length 376;

Best Local Similarity 46.3%; Pred. No. 6e-23;

Matches 68; Conservative 28; Mismatches 45; Indels 6; Gaps 0

QY 47 PMSISALAMVFMGAKNGNTRAQMSQALCKIGGEDGDIHRGFOSLLVAINRTDTEYVL 1

Wed May 28 14:44:10 2003

Db 32 PVSISALAMVLLGAKNGTATQMAQALSIN-----TEEDIHFAFOSLLTEVKNAGTQYLLR 87
Qy 107 TANGLFGEKSDYFLGFTDCGKFKFYQATIKOLDVFNDEKSTTRVNSWADKT--KAWKI 164
Db 88 YANRLFGEKTCQFLSTFKESCLQFYHABLKSLFIRAEEGRKHINTWVSKKTEGKEEL 147
Qy 165 IOTSLSHLEPGIASSCYCKACLSP 191
Db 148 LPSGSDIAETRLVLNVAIFYGKNWEP 174
RESULT 6
SCC2_HUMAN STANDARD; PRT; 390 AA.
ID SCC2_HUMAN AC P48594;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Squamous cell carcinoma antigen 2 (SCCA-2) (Leupin).
GN SERPINB4 OR SCCA2.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95241462; PubMed=7724531;
RA Schneider S.S., Schick C., Fish K.E., Miller E., Pena J.C.,
RA Treter S.D., Hui S.M., Silverman G.A.;
RT "A serine proteinase inhibitor locus at 18q21.3 contains a tandem
RT duplication of the human squamous cell carcinoma antigen gene."
RL Proc. Natl. Acad. Sci. U.S.A. 92:3147-3151(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96013887; PubMed=7589435;
RA Barnes R.C., Worrall D.M.;
RT "Identification of a novel human serpin gene; cloning sequencing and
RT expression of leupin."
RL FEBS Lett. 373:61-65(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21167379; PubMed=11267667;
RA Hamada K., Shimomiyama H., Asano Y., Kihana T., Iwamoto M., Hanakawa Y.,
RA Hashimoto K., Hirose S., Ito M.;
RT "Molecular cloning of human squamous cell carcinoma antigen 1 gene and
RT characterization of its promoter."
RL Biochem. Biophys. Acta 1518:124-131(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone marrow;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY ACT AS A PROTEASE INHIBITOR TO MODULATE THE HOST
CC -1- IMMUNE RESPONSE AGAINST TUMOR CELLS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: SQUAMOUS CELLS.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U19576; AAA92602.1; JOINED.
CC EMBL; U19570; AAA92602.1; JOINED.
CC EMBL; U19571; AAA92602.1; JOINED.
CC EMBL; U19572; AAA92602.1; JOINED.
CC EMBL; U19574; AAA92602.1; JOINED.
CC EMBL; U19575; AAA92602.1; JOINED.
CC EMBL; U19557; AAA97553.1; JOINED.

DR EMBL; X89015; CAA61420.1; --
DR EMBL; AB035089; BAB21525.1; --
DR EMBL; BC017401; AAH17401.1; --
DR HSP; P01008; IATH.
DR Genew; HGNC:10570; SERPINB4.
DR MIM; 600518; --
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin; Serine protease inhibitor.
FT ACT_SITE 354 355 REACTIVE BOND.
SQ SEQUENCE 390 AA; 44854 MW; 04B213CD892587D5 CRC64;
Query Match 23.8%; Score 272; DB 1; Length 390;
Best Local Similarity 38.6%; Pred. No. 2.3e-18;
Matches 54; Conservative 27; Mismatches 47; Indels 12; Gaps 1;
Qy 32 FEKARGKQLQLFFPMSSISALAMVFMGAKNGTAAQMSQALCFSGKIG----- 79
Db 16 FQPRKSKENNIFYSPISITSLGWLGAKDNTAQISKVLHFDQVTEKKAATYHV 75
Qy 80 GEDGDHRRGQSLVAINRTDTBYVLTANGLFGKSYDLTGFTDCGKFKYQATIKOLD 139
Db 76 DRSGNVHVFQKLLTFEKNSTDAVELKIANKLFGEKTYQFLQBYLDAIKKPYQTSVESTD 135
Qy 140 FVNDTEKSTTRVNSWADKT 159
Db 136 FANAPESRRKKINSWVESQT 155
RESULT 7
SCC1_HUMAN STANDARD; PRT; 390 AA.
ID SCC1_HUMAN AC P29508; Q96J21;
DT 01-APR-1993 (Rel. 25, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Squamous cell carcinoma antigen 1 (SCCA-1) (Protein T4-A).
GN SERPINB3 OR SCCA1 OR SCCA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92068241; PubMed=1958219;
RA Suminami Y., Kishi F., Sekiguchi K., Kato H.;
RT "Squamous cell carcinoma antigen is a new member of the serine
RT protease inhibitors."
RL Biochem. Biophys. Res. Commun. 181:51-58(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95241462; PubMed=7724531;
RA Schneider S.S., Schick C., Fish K.E., Miller E., Pena J.C.,
RA Treter S.D., Hui S.M., Silverman G.A.;
RT "A serine proteinase inhibitor locus at 18q21.3 contains a tandem
RT duplication of the human squamous cell carcinoma antigen gene."
RL Proc. Natl. Acad. Sci. U.S.A. 92:3147-3151(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY ACT AS A PROTEASE INHIBITOR TO MODULATE THE HOST
CC -1- IMMUNE RESPONSE AGAINST TUMOR CELLS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: SQUAMOUS CELLS.
CC -1- DEVELOPMENTAL STAGE: ITS EXPRESSION IS CLOSELY RELATED TO CELLULAR
CC DIFFERENTIATION IN BOTH NORMAL AND MALIGNANT SQUAMOUS CELLS.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
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 CC -----

DR EMBL; S66896; AAB20405.1; -
 DR EMBL; U19556; AAA97552.1; -
 DR EMBL; U19568; AAA86317.1; -
 DR EMBL; U19559; AAA86317.1; JOINED.
 DR EMBL; U19560; AAA86317.1; JOINED.
 DR EMBL; U19562; AAA86317.1; JOINED.
 DR EMBL; U19565; AAA86317.1; JOINED.
 DR EMBL; U19567; AAA86317.1; JOINED.
 DR EMBL; U19562; AAA86316.1; -
 DR EMBL; U19559; AAA86316.1; JOINED.
 DR EMBL; U19560; AAA86316.1; JOINED.
 DR EMBL; BC005224; AAA805224.1; -
 DR PIR; JT0966; JT0966.
 DR HSSP; P01008; IATH.
 DR Genew; HGNC:10569; SERPINB3.
 DR MIM; 600517; -
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Serpin; Serine protease inhibitor.
 DR ACT_SITE 354 355 REACTIVE BOND.
 FT CONFLICT 357 357 T -> A (IN REF. 1).
 SO SEQUENCE 390 AA; 44564 MW; 55F27F986C752CFA CRC64;

Query Match 23.28; Score 266; DB 1; Length 390;
 Best Local Similarity 37.94; Pred. No. 8.4e-18;
 Matches 53; Conservative 28; Mismatches 47; Indels 12; Gaps 1;
 32 FEKARGKQLKQILFFPMSSISALAVFMGAKNTAAQMSQALCFSGKIG----- 79
 16 FQPRKSKENNIFYSPTSISALGVLLGAKNTAQIKVLFDFQVNTTGAATYHV 75
 80 GEGDDIHRGQSILVAINRTDTEVLNTANGLFGKSYDFLTGFTDSCGKFFQATIKQLD 139
 76 DRGNVHQFQKLLTEFNKSTDAYELKIANKLFGEKTYLFLQBYLDAIKKFQTSVESVD 135

140 FVNDTEKSTTRVNSWADKT 159
 136 FANAPESRKINSWESQT 155
 ILEU_HORSE STANDARD; PRT; 379 AA.
 AC P05619;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leukocyte elastase inhibitor (LEI).
 GN SERPINB1 OR ELANH2.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93319507; PubMed=7687128;
 RA Kordula T., Dubin A., Schooltink H., Koj A., Heinrich P.C.,
 RA Rose-John S.;
 RT "Molecular cloning and expression of an intracellular serpin: an
 RT elastase inhibitor from horse leukocytes.";
 RL Biochem. J. 293:187-193 (1993).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Leukocyte;

RESULT 8
 ID ILEU_HORSE
 AC P05619;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leukocyte elastase inhibitor (LEI).
 GN SERPINB1 OR ELANH2.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93319507; PubMed=7687128;
 RA Kordula T., Dubin A., Schooltink H., Koj A., Heinrich P.C.,
 RA Rose-John S.;
 RT "Molecular cloning and expression of an intracellular serpin: an
 RT elastase inhibitor from horse leukocytes.";
 RL Biochem. J. 293:187-193 (1993).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Leukocyte;

RA MEDLINE=92202200; PubMed=1551869;
 RA Dubin A., Travis J., Enghild J.J., Potempa J.;
 RT "Equine leukocyte elastase inhibitor. Primary structure and
 RT identification as a thymosin-binding protein.";
 RL J. Biol. Chem. 267:6576-6583 (1992).
 RN [3]
 RP SEQUENCE OF 343-362.
 RX MEDLINE=88213423; PubMed=3366785;
 RX Potempa J., Dubin A., Maronek W., Travis J.;
 RT "An elastase inhibitor from equine leukocyte cytosol belongs to the
 RT serpin superfamily. Further characterization and amino acid sequence
 RT of the reactive center.";
 RL J. Biol. Chem. 263:7364-7369 (1988).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
 RX MEDLINE=92389327; PubMed=1518052;
 RX Baumann U., Bode W., Huber R., Travis J., Potempa J.;
 RT "Crystal structure of cleaved equine leukocyte elastase inhibitor
 RT determined at 1.95-A resolution.";
 RL J. Mol. Biol. 226:1207-1218 (1992).
 CC -!- FUNCTION: THIS INHIBITOR IS THOUGHT TO BE INVOLVED IN THE CONTROL
 CC OF INTRACELLULAR PROTEIN TURNOVER. BINDS TO THYMOSIN BETA-4.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
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DR EMBL; M91161; AAA97513.1; -
 DR PIR; A28060; A28060.
 DR PIR; A37276; A37276.
 DR PIR; A42421; A42421.
 DR PIR; S34062; S34062.
 DR PDB; 1HLE; 31-JAN-94.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Serpin; Serine protease inhibitor; 3D-structure.
 FT MOD_RES 1 1 BLOCKED (WITH AN UNKNOWN CHEMICAL GROUP).
 FT ACT_SITE 344 345 REACTIVE BOND.
 FT HELIX 2 22
 FT STRAND 28 30
 FT HELIX 32 44
 FT TURN 45 45
 FT HELIX 48 58
 FT TURN 59 59
 FT HELIX 60 62
 FT TURN 64 65
 FT HELIX 66 77
 FT TURN 78 78
 FT STRAND 85 95
 FT TURN 96 97
 FT HELIX 102 112
 FT STRAND 115 119
 FT TURN 121 123
 FT HELIX 125 139
 FT TURN 140 142
 FT TURN 150 151
 FT TURN 155 156
 FT STRAND 157 171
 FT HELIX 177 179
 FT STRAND 181 186
 FT STRAND 192 209
 FT HELIX 210 212
 FT TURN 213 213
 FT STRAND 214 221
 FT TURN 222 222

QY 47 PMSISSALAMVFMGAKNTAAQMSQALCFSGKIGGEDGDIHRGFSQSLVAINRTDTEYVLR 106
 Db 32 PFSISSALAMILLGTRGNTAQAQSKALHFDTV---KDIHSRFSQSLNADINKCGASYILK 87
 QY 107 TANGLFGEKSYDFLTGFTDCGKGYQATIKQIDFVNDTEKSTTRVNSWVADTKTKAWLIQ 166
 Db 88 LANRLFGKTYHFLPEFLASTQKTYGAEASVDFLRASEARKAINWVKEQTEG----- 142
 QY 167 TSLSHLEEPGIASSCYCKACLSQPLLVHSI 197
 Db 143 -KIPELLASGWDSA-----TKLVLVNAI 165

RESULT 10
 ILEU HUMAN STANDARD; PRT; 379 AA.
 ID ILEU HUMAN
 AC P30740;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase
 inhibitor) (M/NEI) (EI).
 GN SERPINB1 OR ELANH2 OR P12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 OX [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=92302296; PubMed=1376927;
 RX Remold-O'Donnell E., Chin J., Alberts M.;
 RA "Sequence and molecular characterization of human monocyte/neutrophil
 elastase inhibitor";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:5635-5639(1992).
 RL [2]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=98296265; PubMed=9630619;
 RX Zeng W., Silverman G.A., Remold-O'Donnell E.;
 RA "Structure and sequence of human M/NEI (monocyte/neutrophil elastase
 inhibitor), an Ov-serpin family gene";
 RT Gene 213:179-187(1998).
 RL [3]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Cervix;
 RC Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 178-185; 204-210 AND 364-371.
 RP TISSUE=Keratinocytes;
 RX Rasmussen H.H., van Damme J., Puyse M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 protein database of normal human epidermal keratinocytes";
 RL Electrophoresis 13:960-969(1992).
 CC -!- FUNCTION: REGULATES THE ACTIVITY OF THE NEUTROPHIL PROTEASES
 ELASTASE, CATHEPSIN G AND PROTEINASE-3.
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.

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 EMBL; M91056; NOT ANNOTATED_CDS.
 DR EMBL; AF053630; AAC31394.1;
 DR EMBL; BC009015; A0809015.1;
 DR PIR; S27383; S27383.

FT STRAND 226 233
 FT HELIX 244 248
 FT TURN 249 249
 FT TURN 252 259
 FT HELIX 261 263
 FT STRAND 265 274
 FT STRAND 276 283
 FT STRAND 285 291
 FT TURN 292 292
 FT TURN 295 297
 FT TURN 299 301
 FT TURN 305 308
 FT STRAND 313 326
 FT STRAND 330 343
 FT STRAND 350 353
 FT STRAND 358 364
 FT TURN 365 368
 FT STRAND 369 376
 SQ SEQUENCE 379 AA; 43006 MW; 72DED1999371427A CRC64;

Query Match 22.4%; Score 257; DB 1; Length 379;
 Local Similarity 46.5%; Pred. No. 5.8e-17;
 Matches 53; Conservative 19; Mismatches 38; Indels 4; Gaps 1;

QY 47 PMSISSALAMVFMGAKNTAAQMSQALCFSGKIGGEDGDIHRGFSQSLVAINRTDTEYVLR 106
 Db 32 PFSISSALAMILLGTRGNTAQAQSKALHFDTV---KDIHSRFSQSLNADINKCGASYILK 87
 QY 107 TANGLFGEKSYDFLTGFTDCGKGYQATIKQIDFVNDTEKSTTRVNSWVADTKTK 160
 Db 88 LANRLFGKTYHFLPEFLASTQKTYGAEASVDFLRASEARKAINWVKEQTEG 141

RESULT 9
 ILEU PIG STANDARD; PRT; 378 AA.
 ID ILEU PIG
 AC P80229;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leukocyte elastase inhibitor (LEI) (Leukocyte neutral proteinase
 inhibitor) (LNPI).
 GN SERPINB1 OR ELANH2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 OX [1]
 RP SEQUENCE.
 RP TISSUE=Leukocyte;
 RX MEDLINE=94039085; PubMed=7901009;
 RA Teschauer W.F., Mentele R., Sommerhoff C.P.;
 RT "Primary structure of a porcine leukocyte serpin";
 RL Eur. J. Biochem. 217:519-526(1993).
 CC -!- FUNCTION: REGULATES THE ACTIVITY OF THE NEUTROPHIL PROTEASE
 ELASTASE, CATHEPSIN G AND PROTEINASE-3 (By similarity).
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
 DR HSP; P05619; 1HLE.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin; serine protease inhibitor.
 FT MOD RES 1 1 BLOCKED.
 FT DISULFID 80 80 INTERCHAIN (PROBABLE).
 FT ACT SITE 343 344 REACTIVE BOND (BY SIMILARITY).
 FT SEQUENCE 378 AA; 42512 MW; 3CA7C65F11E508CA CRC64;

Query Match 22.3%; Score 255.5; DB 1; Length 378;
 Best Local Similarity 39.1%; Pred. No. 8e-17;
 Matches 59; Conservative 27; Mismatches 48; Indels 17; Gaps 3;

DR HSP: P05619; 1LHE.
DR Aarhu/Chent-2DPAGE; 4314; IBF.
DR Genw; HGNC:3311; SERPINB1.
DR MIM; 130135; -.
DR InterPro; IPR00215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin; Serine protease inhibitor.
FT ACT SITE 344 345 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 379 AA; 42741 MW; BAAE08DFC8D8CD3 CRC54;

Query Match
Best Local Similarity 21.0%; Score 240; DB 1; Length 379;
Matches 49; Conservative 23; Mismatches 38; Indels 4; Gaps

QY 47 PMSISSALAMVFMGKNGTAAQMSQALCFSGKIGGEDGDIHRFGQSLLVAINRTDTYVLV 106
D 32 PFSSISAMVVLGTRGNTAAQLSKTFHTV-----EVHSRFSQSLNADINKRGASYILK 87
QY 107 TANGLFSGKSYDELGTGFTDSCGKSYQATIIKQLDPVNDEKSTRVNSWVADKTK 160
D 88 LANRLYGKTYNLFPEFLVSTQKTYGADLASVDFQHASDARKNTQWVKGQTE 141

RESULT 11

ID13 HUMAN STANDARD; PRT; 391 AA.

AC Q9UIV8; Q9UBW1; Q9UKG0; Q9HCX1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hurpin (HaCat UV-repressible serpin) (Protease inhibitor 13)
DE (Headpin) (Serpin B13).
GN SERPINB13 OR P113.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Skin;
RX MEDLINE=99443898; PubMed=10512713;
RA Abts H.F., Welles T., Mir mohammadsadeh A., Koehler K., Michel G.,
RA Ruzicka T.;
RT "Cloning and characterization of hurpin (Protease Inhibitor 13): a new
RT skin specific, UV-repressible serine proteinase inhibitor of the
RL ovalbumin serpin family";
RL J. Mol. Biol. 293:29-39(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99458661; PubMed=10527881;
RA Spring P., Nakashima T., Frederick M., Henderson V., Clayman G.;
RT "Identification and cDNA cloning of headpin, a novel differentially
RT expressed serpin that maps to chromosome 18q";
RL Biochem. Biophys. Res. Commun. 264:299-304(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20461850; PubMed=11004515;
RA Nakashima T., Pak S.C., Silverman G.A., Spring P.M., Frederick M.J.,
RA Clayman G.L.;
RT "Genomic cloning, mapping, structure and promoter analysis of HEADPIN,
RT a serpin which is down-regulated in head and neck cancer cells";
RL Biochim. Biophys. Acta 1492:441-446(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=21213570; PubMed=11313015;
RA Abts H.F., Welles T., Scheuring S., Scott F.L., Irving J.A., Michel G.,
RA Bird P.I., Ruzicka T.;
RT "Sequence, organization, chromosomal localization and alternative
RT splicing of the human serine protease inhibitor gene hurpin (P113),
RT which is up-regulated in psoriasis";

CC	CELL-DERIVED PAI-1.	
CC	-!- SUBCELLULAR LOCATION: CYTOPLASMIC OR EXTRACELLULAR.	
CC	-!- PTM: THE SIGNAL SEQUENCE IS NOT CLEAVED.	
CC	-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.	
CC		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC		
CC	EMBL: J02685; AAA36413.1; -	
DR	EMBL: M18082; AAA60006.1; -	
DR	EMBL: Y00630; CAA68666.1; -	
DR	EMBL: M24657; AAA60348.1; -	
DR	EMBL: M24651; AAA60348.1; JOINED.	
DR	EMBL: M24652; AAA60348.1; JOINED.	
DR	EMBL: M24653; AAA60348.1; JOINED.	
DR	EMBL: M24654; AAA60348.1; JOINED.	
DR	EMBL: M24655; AAA60348.1; JOINED.	
DR	EMBL: M24656; AAA60348.1; JOINED.	
DR	EMBL: J03603; AAA60004.1; -	
DR	EMBL: M31551; AAA36797.1; -	
DR	EMBL: M31547; AAA36797.1; JOINED.	
DR	EMBL: M31548; AAA36797.1; JOINED.	
DR	EMBL: M31549; AAA36797.1; JOINED.	
DR	EMBL: M31550; AAA36797.1; JOINED.	
DR	EMBL: BC012609; AAA12609.1; -	
DR	EMBL: A21238; CAA01535.1; -	
DR	EMBL: A21254; CAA01539.1; -	
DR	PIR: A26553; A26553.	
DR	PIR: A29362; A29362.	
DR	PIR: A32853; A32853.	
DR	PIR: A31366; A31366.	
DR	PDB: 1BY7; 24-OCT-99.	
DR	Aarhus/Ghent-2DPAGE; 6314; IEF.	
DR	Genew; HGNC:8584; SERPIN2.	
DR	MIN; 173390; -	
DR	InterPro; IPR000215; Serpin.	
DR	Pfam; PF000079; serpin; 1.	
DR	SMART; SMO0093; SERPIN; 1.	
DR	PROSITE; PS00284; SERPIN; 1.	
DR	Serpin; Serine protease inhibitor; plasma; plasminogen activation;	
KW	Glycoprotein; signal; 3D-structure; Polymorphism.	
KW	SIGNAL 1 NOT CLEAVED.	
FT	CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD 115 115 N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	ACT SITE 380 381 REACTIVE BOND.	
FT	VARIANT 120 120 N -> D (IN DBSNP:6098).	
FT	/FTID=VAR 011743.	
FT	VARIANT 404 404 N -> K (IN DBSNP:6103).	
FT	/FTID=VAR 011744.	
FT	VARIANT 413 413 S -> C (IN DBSNP:6104).	
FT	/FTID=VAR 011745.	
FT	CONFLICT 170 170 N -> Y (IN REF. 7).	
FT	SEQUENCE 415 AA; 46596 MW; 10DFAB5A4B1246FF CRC64;	
SQ		
	Query Match 19.3%; Score 221.5; DB 1; Length 415;	
	Best Local Similarity 32.1%; Pred. No. 1.5e-13;	
	Matches 51; Conservative 27; Mismatches 48; Indels 33; Gaps	
QY	35 ARGKQLKQLIFFPMGSISSALAMVFMKAGNTAAQMSQALCFKSGK----- 79	
Db	20 AKASPTQNLFLSPWSISSTMAVMYSGRSTEDQMAKVLQFNVEGANAVTMTPTNFTSC 79	
QY	80 -----CEDGD-----IHRGQSLLVALNRDTEVLFRTANGLFGEKSYDFLT 121	
Db	80 GFNQIQTKSGYFDAILQAQAADKIHSFRSLSSAINASTGNVLLSVNKLFGKSAASPRE 139	
QY	122 GFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADTKY 160	

Db 140 EYRLCQYSSSEPOAVDFLECAEARKINSWVKTK 178
 RESULT 13
 PA12 MOUSE
 ID PA12 MOUSE STANDARD; PRT; 415 AA.
 AC P12388; Q35687; Q9QWZ5; Q9QWQ0; Q9QWP9; Q9QWP8; Q9QWP7;
 AC Q9QWP6;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Plasminogen activator inhibitor-2, macrophage (PAI-2).
 GN SERPINB2 OR PAI2 OR PLAH2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX [1]
 RC SEQUENCE OF 1-27 FROM N.A.
 RC STRAIN=AKR; TISSUE=Myeloid;
 RX MEDLINE=90059920; PubMed=2583099;
 RA Belin D., Wohlwend A., Schleuning W.-D., Kruithof E.K.O.,
 RA Vassalli J.-D.;
 RT "Facultative polypeptide translocation allows a single mRNA to encode
 RT the secreted and cytosolic forms of plasminogen activators inhibitor
 RT 2.";
 RL EMBO J. 8:3287-3294 (1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AKR; TISSUE=Myeloid;
 RA Belin D.;
 RL Submitted (SEP-1989) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS GLU-239; TYR-258; ILE-259, AND
 RP ARG-284.
 RC STRAIN=129; TISSUE=Liver;
 RA Belin D., Tapparel C., Sappino N., Silva P.;
 RL "Sequence and tissue-specific expression of the murine PAI-2 gene.";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-34; 54-74; 89-115; 124-156; 163-237 AND 265-302 FROM
 RP N.A.
 RC STRAIN=129/Sv;
 RX MEDLINE=99110951; PubMed=9892694;
 RA Dougherty K.M., Pearson J.M., Yang A.Y., Westrick R.J., Baker M.S.,
 RA Glinesburg D.;
 RL "The plasminogen activator inhibitor-2 gene is not required for normal
 RL murine development or survival.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:686-691 (1999).
 CC -1- FUNCTION: PAI-2 inhibits urokinase-type plasminogen activator. The
 CC monocyte derived PAI-2 is distinct from the endothelial cell-
 CC derived PAI-1. Not required for normal murine development or
 CC survival.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC OR EXTRACELLULAR.
 CC -1- PTM: THE SIGNAL SEQUENCE IS NOT CLEAVED.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
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 CC -----
 DR EMBL; X16490; CAA34507.1; -
 DR EMBL; AJ000386; CAA04047.1; -
 DR EMBL; AJ000384; CAA04047.1; JOINED.
 DR EMBL; AJ000385; CAA04047.1; JOINED.
 DR EMBL; AF069683; AAD08915.1; -
 DR EMBL; AF069685; AAD08916.1; -
 DR EMBL; AF069684; AAD08916.1; JOINED.

DR EMBL; AF069687; AAD08917.1; -
 DR EMBL; AF069686; AAD08917.1; JOINED.
 DR EMBL; AF069689; AAD08918.1; -
 DR EMBL; AF069688; AAD08918.1; JOINED.
 DR EMBL; AF069690; AAD08919.1; -
 DR EMBL; AF069692; AAD08920.1; -
 DR EMBL; AF069691; AAD08920.1; JOINED.
 DR EMBL; AF069693; AAD08921.1; -
 DR PIR; S09615; S09616.
 DR PIR; S20047; S20047.
 DR HSSP; P05120; 1BY7.
 DR MGD; MGI:97609; Serpinb2.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin; Serine protease inhibitor; Plasma; Plasminogen activation;
 KW Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 ? NOT CLEAVED.
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT ACT SITE 380 381 REACTIVE BOND.
 FT VARIANT 239 239 A -> E.
 FT VARIANT 258 258 H -> Y.
 FT VARIANT 259 259 T -> I.
 FT VARIANT 284 284 S -> R.
 FT CONFLICT 55 55 A -> T (IN REF. 3 AND 4).
 SQ SEQUENCE 415 AA; 46291 MW; C4FC78C5C3CA7D8B CRC64;
 Query Match 18.9%; Score 216.5; DB 1; Length 415;
 Best Local Similarity 32.7%; Pred. No. 4.5e-13;
 Matches 54; Conservative 23; Mismatches 53; Indels 35; Gaps 3;
 Qy 29 IKPEKARGKQLKQLIFFPMSISSALAMVPMGAKGNTAAQMSOALCFSGKIG----- 79
 Db 16 LKQIEKNSNTQ--NIFSPWSISSTLAIIVLLGAGGNTQQQMAKVLFQFNEIGSYGITRNP 73
 Qy 80 -----GEDGD-IHRGFQSLVAINRTDTETVLRVLTANGLFGEK 115
 Db 74 ENFSGCDFAQIQENYPSAILQAQAGDKIHSAFSSLSSTINTPOGDYLLSANKLFGEK 133
 Qy 116 SYDFLTGFTDSCGKGYOATIKQLDFVNDTEKSTTRVNSWVADTK 160
 Db 134 SARFKEEYQLSKYYSTPEPEAVDFLECAEAREKINSWVKTK 178
 RESULT 14
 SB10 HUMAN
 ID SB10 HUMAN STANDARD; PRT; 397 AA.
 AC P48595;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Bompapin (Protease inhibitor 10) (serpin B10).
 GN SERPINB10 OR PI10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=96070759; PubMed=7592909;
 RA Riewald M., Schleef R.R.;
 RT "Molecular cloning of bompapin (protease inhibitor 10), a novel human
 RT serpin that is expressed specifically in the bone marrow.";
 RL J. Biol. Chem. 270:26754-26757 (1995).
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF PROTEASE
 CC ACTIVITIES DURING HEMATOPOIESIS.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

Search completed: May 20, 2003, 10:24:21
Job time : 16 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 20, 2003, 10:19:47 ; Search time 84 seconds
(without alignments)
527.382 Million cell updates/sec

Title: US-09-912-628-7

Perfect score: 1145

Sequence: 1 HELSWAARRTCAHRGCS.....SIPKNSPVTPHGMXPPSL 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Spaced: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	377.5	33.0	377	11 O08804	O08804 mus musculus
2	347.5	30.3	385	11 Q8VHQ0	Q8VHQ0 mus musculus
3	344	30.0	374	11 O08800	O08800 mus musculus
4	272	23.8	369	4 Q8BYF7	Q8BYF7 homo sapien
5	266	23.2	338	4 Q8BYF8	Q8BYF8 homo sapien
6	259	22.6	374	11 O08797	O08797 mus musculus
7	251.5	22.0	382	11 Q8VHP7	Q8VHP7 mus musculus
8	249.5	21.8	377	11 O08806	O08806 mus musculus
9	248.5	21.7	377	11 Q9DAZ7	Q9DAZ7 mus musculus
10	248.5	21.7	377	11 Q8VHQ1	Q8VHQ1 mus musculus
11	245	21.4	387	11 Q9DIQ5	Q9DIQ5 mus musculus
12	243	21.2	379	11 Q9DOS8	Q9DOS8 mus musculus
13	243	21.2	379	11 Q9DI54	Q9DI54 mus musculus
14	240	21.0	377	11 Q9DAV6	Q9DAV6 mus musculus
15	237	20.7	379	11 Q9D7S8	Q9D7S8 mus musculus
16	225.5	19.7	388	11 Q9Z2G2	Q9Z2G2 mus musculus

17	210	18.3	410	13	O73790	gallus gall
18	204	17.8	359	11	Q9D6A7	mus musculus
19	196.5	17.2	386	11	Q9D1E7	mus musculus
20	194	16.9	421	6	O46519	mus musculus
21	191.5	16.7	413	11	Q8VC20	mus musculus
22	190.5	16.6	410	11	Q8VH5	mus musculus
23	190.5	16.6	413	11	Q8VC41	mus musculus
24	190.5	16.6	413	11	Q91V74	mus musculus
25	188.5	16.5	418	11	Q03734	mus musculus
26	187.5	16.4	388	11	Q9CQV3	mus musculus
27	187.5	16.4	388	11	Q91Z12	mus musculus
28	187.5	16.4	418	11	Q62257	mus musculus
29	187	16.3	423	11	Q9D7P9	mus musculus
30	186.5	16.3	380	11	Q920075	mus musculus
31	186.5	16.3	413	11	Q91XB8	mus musculus
32	186.5	16.3	418	11	Q62258	mus musculus
33	186.5	16.3	418	11	Q91WP6	mus musculus
34	186.5	16.3	425	11	Q91XC1	mus musculus
35	185	16.2	406	11	Q64118	mus musculus
36	184.5	16.1	418	11	Q91XB0	mus musculus
37	184.5	16.1	418	11	Q8VCH3	mus musculus
38	184	16.1	418	5	Q27085	tachypleus
39	183.5	16.0	413	11	Q63969	mus baxicol
40	182.5	15.9	380	11	Q9D695	mus musculus
41	182.5	15.9	418	11	Q91W80	mus musculus
42	182	15.9	396	6	O00394	cercopithec
43	182	15.9	413	11	O54761	spermophilu
44	180.5	15.8	433	13	Q9YIB8	xenopus lae
45	179	15.6	413	6	Q28666	oryctolagus

ALIGNMENTS

RESULT 1

ID	O08804	PRELIMINARY;	PRT;	377 AA.
AC	O08804;			
DT	01-JUN-1997 (TRENBLrel. 04, Created)			
DT	01-DEC-2001 (TRENBLrel. 19, Last sequence update)			
DT	01-JUN-2002 (TRENBLrel. 21, Last annotation update)			
DE	Serine proteinase inhibitor NK13.			
GN	SP112.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL;			
RX	MEDLINE=97326124; PubMed=9182575;			
RA	Sun J., Ooms L., Bird C.H., Sutton V.R., Trapani J.A., Bird P.I.;			
RT	"A new family of 10 murine ovalbumin serpins includes two homologs of			
RT	proteinase inhibitor 8 and two homologs of the granzyme B inhibitor			
RT	(proteinase inhibitor 9).";			
RL	J. Biol. Chem. 272:15434-15441(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL;			
RA	Kaiserman D., Knaggs S., Scarff K.L., Gillard A., Mirza G., Cadman M.,			
RA	McKeone R., Denny P., Cooley J., Benarafa C., Remold-O'Donnell E.,			
RA	Ragoussis J., Bird P.I.;			
RT	"Comparison of human chromosome 6p25 with murine chromosome 13 reveals			
RT	a greatly expanded Ov-serpin gene repertoire in the mouse.";			
RL	Submitted (SEP-2001) to the EMBL/genbank/DBJ databases.			
CC	-1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.			
DR	EMBL; U96707; AAB57819.2; -			
DR	MGI; MGI:894688; Sp112.			
DR	InterPro; IPR000215; Serpin.			
DR	Pfam; PF00079; serpin; 1.			
DR	SMART; SM00093; SERPIN; 1.			
DR	PROSITE; PS00284; SERPIN; 1.			
KW	Serpin.			

SEQUENCE 377 AA; 42535 MW; 9660E8F3A41EE47A CRC64;

Query Match 33.0%; Score 377.5; DB 11; Length 377;
Best Local Similarity 50.7%; Pred. No. 2.5e-29;
Matches 75; Conservative 29; Mismatches 41; Indels 3; Gaps 2;

QY 41 KQLIFFPMISSSALAMVFMGAKNTAAQMSQALCFSGIGEDG-DIHRGFQSLLVAINT 99
DBB 25 RNVLFSPISVSALAMVFMGAKTASQAQALSLDKCSKGGRDVHQGFQSLLTETNKT 84

QY 100 DTEYVLRTANGLFGEKSYDFLGTFTDSCCKPQOATIKOLDVNDPEKSTRVNSWADTK 159
DBB 85 GTQYVLRTANRLFGEKTFDILASFDCSKFYAEEMELDFKGATEQSRQHINAWAVAKT 144

QY 160 --KAWKIQTSLSHLEEPGIASSCYCK 185
DBB 145 EDKITELSSGSVSNTPILVNAIYFK 172

RESULT 2

QY 0 PRELIMINARY; PRT; 385 AA.

AC Q8VHQ0;

DT 01-NAR-2002 (TREMBLrel. 20, Created)

DT 01-WAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE SPI312.

GN SPI312.

OC Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=B6D2 F1/J;

RA Kaiserman D., Knaggs S., Scarff K.L., Gillard A., Mirza G., Cadman M.,
RA McKeone R., Denny P., Cooley J., Benarafa C., Remold-O'Donnell E.,
RA Ragoussis J., Bird P.I.;
RA "Comparison of Human Chromosome 6p25 with Murine Chromosome 13 Reveals
RT a Greatly Expanded Ov-Serpin Gene Repertoire in the Mouse.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL ENBL; AF425084; AAL65910.1; -
DR Interpro; IPR000215; Serpin.
DR PFam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN 1.
SQ SEQUENCE 385 AA; 43786 MW; 0820A8A26AEBB485 CRC64;

Query Match 30.3%; Score 347.5; DB 11; Length 385;
Best Local Similarity 48.0%; Pred. No. 2.5e-26;
Matches 71; Conservative 25; Mismatches 49; Indels 3; Gaps 2;

QY 41 KQLIFFPMISSSALAMVFMGAKNTAAQMSQALCFSKI-GGEDGDHHRGFQSLLVAINT 99
DBB 25 KNVFLSPISVSALMVLVGAKGTITAIQTALSLGKCSSSESDGVHQGFQSLTSEVNTK 84

QY 100 DTEYVLRTANGLFGEKSYDFLGTFTDSCCKPQOATIKOLDVNDPEKSTRVNSWADTK 159
DBB 85 GTQYSLKAANRLFGEKTFDILASFDCSKFYAEEMELDFKGATEQSRQHINAWAVAKT 144

QY 160 --KAWKIQTSLSHLEEPGIASSCYCK 185
DBB 145 EDKITELSSPGTIHSNTPILVNAVYFK 172

RESULT 3

ID O08800 PRELIMINARY; PRT; 374 AA.

AC O08800;

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update);


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SQ SEQUENCE 369 AA; 42287 MW; CED7A2426378DE3E CRC64;
Query Match 23.8%; Score 272; DB 4; Length 369;
Best Local Similarity 38.6%; Pred. No. 8.4e-19;
Matches 54; Conservative 27; Mismatches 47; Indels 12; Gaps 1;

Qy 32 FEKARGKQLKQLFFPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIG----- 79
Db 16 FQFRKSKENNIFYSPISITSA LGVLLGAKDNTAQQISKVLHPDQVTENTTEKAATYHV 75
Qy 80 GEDGDIHRGFQSLLLVAINTDTEYVLRTANGLFGKSKSYDLTGFTDSCGKFQATIKQLD 139
Db 76 DRSGNVHHQFQKLLTFEFNKSTDAYELKIANKLFGKTYLFLQEYLDIAKKFYQTSVESTD 135
Qy 140 FVNDTEKSTTRVNSWADKT 159
Db 136 FANAPESRKINSWVESQT 155

R 5
Q 8
AC Q9BYF8 PRELIMINARY; PRT; 338 AA.
ID Q9BYF8;
AC Q9BYF8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE SCALb.
GN SCAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RA Suminami Y., Kishi F., Murakami A., Sakaguchi Y., Kato H.;
RT "Novel Forms of SCC Antigen Transcripts Produced by Alternative
RT Splicing.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AB046399; BAB40772.1;
DR HSSP; P01008; 1ATH.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW SERPIN.
SQ SEQUENCE 338 AA; 38519 MW; 5AB9CEFA80C1ABDF CRC64;
Query Match 23.2%; Score 266; DB 4; Length 338;
Best Local Similarity 37.9%; Pred. No. 3e-18;
Matches 53; Conservative 28; Mismatches 47; Indels 12; Gaps 1;

Qy 32 FEKARGKQLKQLFFPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIG----- 79
Db 16 FQFRKSKENNIFYSPISITSA LGVLLGAKDNTAQQIKKVLHPDQVTENTTGAATYHV 75
Qy 80 GEDGDIHRGFQSLLLVAINTDTEYVLRTANGLFGKSKSYDLTGFTDSCGKFQATIKQLD 139
Db 76 DRSGNVHHQFQKLLTFEFNKSTDAYELKIANKLFGKTYLFLQEYLDIAKKFYQTSVESTD 135
Qy 140 FVNDTEKSTTRVNSWADKT 159
Db 136 FANAPESRKINSWVESQT 155

R 5
Q 8
AC Q08797 PRELIMINARY; PRT; 374 AA.
ID Q08797;
AC Q08797;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Serine proteinase inhibitor 6.

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Wed May 28 14:44:11 2003

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Db 28 IFFSPFSSSLAMVFLGKAGSTRAQLSKTLHFDV-----EDHSCFOSLTAEVSKLGAS 83
Qy 103 YVLRANGFGEKSYDFLTGFTDSCGKYQATIKOLDPVDNTEKSTTRVNSWVADTKAW 162
Db 84 HTLKLARLYGKTYNLFPEFLASTQKYSADLAADVDFQHASDARKEINQWVGQTEG- 142
Qy 163 KIIQTSLSHLEPPGIASSSCYKACLSOPLLVHSI 197
Db 143 -----KIPPELLAGVDS-----MTKLVLVNAI 165

RESULT 8
O0806 PRELIMINARY; PRT; 377 AA.
AC O0806
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Serine proteinase inhibitor NK26.
GN SPI14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=ECTOPLACENTAL CONE;
RX MEDLINE=9726124; PubMed=9182575;
RA Sun J., Coms L., Bird C.H., Sutton V.R., Trapani J.A., Bird P.I.;
RA "A new family of 10 murine ovalbumin serpins includes two homologs of
RT proteinase inhibitor 8 and two homologs of the granzyme B inhibitor
RT [proteinase inhibitor 9].";
RL J. Biol. Chem. 272:15434-15441 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=ECTOPLACENTAL CONE;
RA Kaiserman D., Knaggs S., Scarff K.L., Giffard A., Mirza G., Cadman M.,
RA McKeone R., Denny P., Cooley J., Benarafa C., Remold-O'Donnell E.,
RA Ragoussis J., Bird P.I.;
RA "Comparison of human chromosome 6p25 with murine chromosome 13 reveals
RT a greatly expanded Ov-serpin gene repertoire in the mouse.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -/- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; U96709; AAB57821.2; -.
DR MGD; MGI:894672; Spi14.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
SQ SEQUENCE 377 AA; 42783 MW; EC8C2D7991682B4F CRC64;
Query Match 21.8%; Score 249.5; DB 11; Length 377;
Best Local Similarity 45.5%; Pred. No. 1.5e-16;
Matches 55; Conservative 21; Mismatches 40; Indels 5; Gaps 2;

Qy 41 KOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFSQSLVAINRTD 100
Db 26 ENVCYSPMSISSALAMVLLGAGDTAVQICQALHLN-----PDEVHGFQQLLNKNPN 81

Qy 101 TE-VYLRANGFGEKSYDFLTGFTDSCGKYQATIKOLDPVDNTEKSTTRVNSWVADTK 159
Db 82 NQYCLTWANRLFVENTCELLPTFKSKLKYHSEIQLSFAEAESRQHINMWVSKQT 141

Qy 160 K 160
Db 142 K 142

RESULT 9
Q9DAZ7 PRELIMINARY; PRT; 377 AA.
AC Q9DAZ7
Qy 9
Db 9

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DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 1600002F03RIK protein.
GN 1600002F03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PLACENTA;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
CC -/- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AK005394; BAB23998.1; -.
DR HSSP; P05120; 1BY7.
DR MGD; MGI:1919260; 1600002F03RIK.
DR InterPro; IPR000240; Maspin.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PRINTS; PR00676; MASPIN.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin.
SQ SEQUENCE 377 AA; 43025 MW; CD162840210BE40D CRC64;
Query Match 21.7%; Score 248.5; DB 11; Length 377;
Best Local Similarity 45.0%; Pred. No. 1.9e-16;
Matches 54; Conservative 22; Mismatches 39; Indels 5; Gaps 2;

Qy 41 KOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFSQSLVAINRTD 100
Db 26 KNCVCSPMSSISSALAMVLLGAGDTAVQICQALHLN-----PDEVHGFQQLLNKNQN 81

Qy 101 TE-VYLRANGFGEKSYDFLTGFTDSCGKYQATIKOLDPVDNTEKSTTRVNSWVADTK 159
Db 82 NQYCLTWANRLFVENTCELLPTFKSKLKYHSEIQLSFAEAESRQHINMWVSKQT 141

RESULT 10
Q8VHQ1 PRELIMINARY; PRT; 377 AA.
ID Q8VHQ1
AC Q8VHQ1;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE NK21L1.
GN NK21L1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=ECTOPLACENTAL CONE;
RA Katserman D., Knaggs S., Scarff K.L., Gillard A., Mirza G., Cadman M.,
RA McKeone R., Denny P., Cooley J., Benarafa C., Remold-O'Donnell E.,
RA Ragousis J., Bird P.I.;
RT "Comparison of Human Chromosome 6p25 with Murine Chromosome 13 Reveals
RL a Greatly Expanded Ov-Serpin Gene Repertoire in the Mouse.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF425083; AAL65909.1; -
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN 1.
SQ SEQUENCE 377 AA; 42994 MW; CCA62840210B540D CRC64;

Query Match 21.7% Score 248.5; DB 11; Length 377;
Best Local Similarity 45.0%; Pred. No. 1.9e-16;
Matches 54; Conservative 22; Mismatches 39; Indels 5; Gaps

Q 41 KQLIFFPMSISSALAMVFMCAKGNTRAQMSQALCFKICGEGDGHROFSQLLVAINRTD 100
D 26 KNVCYSPTSISALAMVLLCAKGGTAVQICQALHLN----PDVDYHQGFQLLNLNKNQ 81

Qy 101 TE-VYLRTANGLFGKESYDLFTGTDSCGKGYQATIKQLDFVNDTEKGTTRVNSWVADKT 159
Db 82 NQKYCLTMANRLFVENTCELLPTFKESCLKFYHSEMEQLSFAPAAEESRQHINMWSKQT 141

RESULT 11
Q9D1Q5 PRELIMINARY; PRT; 387 AA.
AC Q9D1Q5
CT Q9D1Q5
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 18 days embryo cDNA, RIKEN full-length enriched library,
DE clone:rl10001H02, full insert sequence.
GN SCCA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Izawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavita H.,
RA Frieschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsumoto Y., Nishida I., Peele G., Quackenbush J.,
RA Schriml L.M., Staublei F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC EMBL; AK003220; BAB22650.1; -
DR HSP; P05120; 1B7.
DR MGD; MGI:1277952; Scca2.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.

```

SQ SEQUENCE 379 AA; 42575 MW; F492F1EB8880B1 CRC64;
 Query Match 21.2%; Score 243; DB 11; Length 379;
 Best Local Similarity 34.5%; Pred. No. 6.9e-16; Indels 24; Gaps 4;
 Matches 58; Conservative 32; Mismatches 54;

QY 43 LIFPMSISSALAWPMGAKNTAAQMSQALCFSGKIGDGDHHRGFSQSLLVAINRTDTE 102
 Db 28 IFFSPFSSISSALAWVILGAKGSTAAQLSKTFHDSV----EDIHSRFQSLNAEVSXRGAS 83
 QY 103 YVLRRTANGLFGEKSYDFTLTGDCGKYQATIKQLDFVNDTEKSTTRVNSVADTKAW 162
 Db 84 HTLKLNLRYGKTYNLFPEYLASTQKMGADLAPVDFLHASEDARKKEINQWVGQTEG- 142
 QY 163 KIIQTSLSHLEBPGIASSCYCKACLSQPLLVHSIPKCNSPVTPHGMW 210
 Db 143 -----KIPKLLSVGVVNS-----MTKLVLVNAI-----YFKGMW 171

RESULT 13
 Q9D154 PRELIMINARY; PRT; 379 AA.
 ID Q9D154
 AC Q9D154
 DT 01-JUN-2001 (TREMELrel. 17, Created)
 DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE 1190005M04RIK protein (RIKEN cDNA 1190005M04 gene) (ETA).
 GN SERPINB1 OR 1190005M04RIK OR SERPINB1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schraml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=SPLEEN;
 RA Kalserman D., Knaggs S., Scarff K.L., Gillard A., Mirza G., Cadman M.,
 RA McKeone R., Denny P., Cooley J., Benarafa C., Remold-O'Donnell E.,
 RA Ragoussis J., Bird P.I.;
 RT "Comparison of human chormosome 6p25 with murine chromosome 13 reveals
 RT a greatly expanded Ov-serpin gene repertoire in the mouse."
 RL Genomics 0:0-0(2002).
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; AK003930; BAB23079.1; -;
 DR EMBL; BC011140; AAL11140.1; -;
 DR EMBL; AF426024; AAL57486.1; -;
 DR HSSP; P05619; 1HLE.
 DR MGD; MGI:1913472; Serpinb1a.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 W Serpin.

SQ SEQUENCE 379 AA; 42575 MW; F492F1EB8880B1 CRC64;
 Query Match 21.2%; Score 243; DB 11; Length 379;
 Best Local Similarity 34.5%; Pred. No. 6.9e-16; Indels 24; Gaps 4;
 Matches 58; Conservative 32; Mismatches 54;

QY 43 LIFPMSISSALAWPMGAKNTAAQMSQALCFSGKIGDGDHHRGFSQSLLVAINRTDTE 102
 Db 28 IFFSPFSSISSALAWVILGAKGSTAAQLSKTFHDSV----EDIHSRFQSLNAEVSXRGAS 83
 QY 103 YVLRRTANGLFGEKSYDFTLTGDCGKYQATIKQLDFVNDTEKSTTRVNSVADTKAW 162
 Db 84 HTLKLNLRYGKTYNLFPEYLASTQKMGADLAPVDFLHASEDARKKEINQWVGQTEG- 142
 QY 163 KIIQTSLSHLEBPGIASSCYCKACLSQPLLVHSIPKCNSPVTPHGMW 210
 Db 143 -----KIPKLLSVGVVNS-----MTKLVLVNAI-----YFKGMW 171

RESULT 14
 Q9DAV6 PRELIMINARY; PRT; 377 AA.
 ID Q9DAV6
 AC Q9DAV6; O08802;
 DT 01-JUN-2001 (TREMELrel. 17, Created)
 DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE 1600019A21RIK protein (Serine proteinase inhibitor R86).
 GN 1600019A21RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PLACENTA;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schraml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=WHOLE EMBRYO;
 RX MEDLINE=97326124; PubMed=9182575;
 RA Sun J., Ooms L., Bird C.H., Sutton V.R., Trapani J.A., Bird P.I.;
 RT "A new family of 10 murine ovalbumin serpins includes two homologs of
 RT proteinase inhibitor 8 and two homologs of the granzyme B inhibitor
 RT (proteinase inhibitor 9)."
 RL J. Biol. Chem. 272:15434-15441(1997).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=WHOLE EMBRYO;
 RA Kalserman D., Knaggs S., Scarff K.L., Gillard A., Mirza G., Cadman M.,
 RA McKeone R., Denny P., Cooley J., Benarafa C., Remold-O'Donnell E.,
 RA Ragoussis J., Bird P.I.;
 RT "Comparison of human chromosome 6p25 with murine chromosome 13 reveals
 RT a greatly expanded Ov-serpin gene repertoire in the mouse."

Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

EMBL; AK005491; BAB24076.1; --
 DR EMBL; U96705; AAB57817.2; --
 DR HSP; P05619; LHLE
 DR MGD; MG1.1919261; 1600019A21R1k.
 DR InterPro; IPR000240; Serpin.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR PRINTS; PRO0676; MASPIN.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin.

SQ SEQUENCE 377 AA; 42733 MW; B6DCCAE1ADE932F4 CRC64;

Query Match 21.0%; Score 240; DB 11; Length 377;

Best Local Similarity 43.3%; Pred No. 1.4e-15;
 Matches 52; Conservative 24; Mismatches 40; Indels 4; Gaps 1;

QY 41 KQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLVAINRTD 100

Db 26 KNVCFSPVSISSALAMVLLGAEQTAVQISQALGLKKEG----IHQGFLLKLLRLINKED 81

QY 101 TEVLRTANGLFGEKSYDFTLTGFTDCGKFKYQATIKQLDFVNDTEKSTTRVNSWVADTKY 160

Db 82 RKYSLLVANRLFADKTCVLTQTFKSCFRFDSEMEQVNFKAQVESRQCINTVWSKQTE 141

RESULT 15

Q9D7S8
 ID Q9D7S8 PRELIMINARY; PRT; 379 AA.
 AC Q9D7S8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 1190005M04Rik protein.
 GN SERPINB1A OR 1190005M04RIK.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=STOMACH;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Izawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Aito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
 RA Hayaebizaki Y.,
 FT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).

-1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

EMBL; AK008914; BAB25964.1; --

DR HSP; P05619; LHLE

DR MGD; MG1.1913472; SerpinB1a.

DR InterPro; IPR000215; Serpin.

DR Pfam; PF00079; serpin; 1.

DR SMART; SM00093; SERPIN; 1.

DR PROSITE; PS00284; SERPIN; 1.

KW Serpin.
 SQ SEQUENCE 379 AA; 42580 MW; 193728585077AB4B CRC64;

Query Match 20.7%; Score 237; DB 11; Length 379;
 Best Local Similarity 33.9%; Pred No. 2.7e-15;
 Matches 57; Conservative 32; Mismatches 55; Indels 24; Gaps 4;

QY 43 LIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSGKIGGEDGDIHRGFQSLVAINRTDTE 102

Db 28 IFFSPFSSISSALAMVILGAKGSTAAQLSKTFHFDSV----EDIHSRFQSQNAEVSQRGAS 83

QY 103 YVLRRTANGLFGEKSYDFTLTGFTDCGKFKYQATIKQLDFVNDTEKSTTRVNSWVADTKAW 162

Db 84 HTLKLANRLYGEKTYNLFPEYLASTQKMYGADLAPVDFLHASEDARKEINQWVKQTEG- 142

QY 163 KIIQTSLSHLBEPGIASSCYCKACLSQLLVHSIPKCNPSVTPHGMW 210

Db 143 -----KIPELLSVGVVDS-----MTKLVLVNAI-----YPKGMW 171

Search completed: May 20, 2003, 10:25:54
 Job time : 88 secs

